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This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

This corresponds to the amino acid sequence <SEO ID 2012; ORF 627>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

```

              10      20      30      40      50      60
m627.pep      MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g627           MSGLWKPEHPGFEILGSRYALQNLVRDVILITLAVSMAITPKQVRAGNEFNFEPIAEVG
              10      20      30      40      50      60

```


1002

	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVS LVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVS LVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATCTT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCTCG TTTCATTTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAGGCC ATTGCCGAAC AGCGGGCGGT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCTCTG CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

a627.pep	1	MSG	LWK	PEHP	GFE	ILG	SRYA	LQN	LVR	DVIL	IAL	TAV	SMAI	TPK	QVR	AGNE
	51	FNFE	PIAE	VG	KLFL	GIFIT	IFPV	LSIL	KAG	EAG	ALGG	VVS	LVH	D	TAG	HP
	101	NVM	YFW	MSGI	LSA	FLDN	APT	YLV	FFN	MAGG	DAQ	ALMT	GSL	FHS	LLAV	SMG
	151	SVFM	GALTY	GNAP	NFM	VKA	IAE	QRG	VPMP	TFF	GYMM	WSV	AFL	TPV	FIVH	
	201	TLIFF	VFKLL	*												

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGWLKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGWLKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVS LVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVS LVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
 190 200 210

g628.seq

```
1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
101 ACACATGGAT TTTACGTTTC GTACGGCGGC TCAATACCAA CAGGCCGCGT
151 TTGAAGTCTT CGGCGGTTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
301 GATTGAATCA GGTTCGGCGC CACTTTTTTC CTGCTCAATT TTGCCAGCGC
351 TTCAGGTacg TAG
```

g628.pep

1	MCVPLKPAGC	GPPNSCVSIL	AAFSDGTSAP	<u>AALHTWILRS</u>	VRRLLNTNRPR
51	LKSSAASLMM	TVGSAASGLV	<u>SIALTKMANG</u>	SASTAGILLN	GRVRSVAVHKP
101	D*IRLRRTFS	LLNFASASGT	*		

```
m628.seq
  1  ATGTGCGTGC  CACTCAAACC  GGCAGGATGC  GGCCCGCCA  ATTCATGTGT
51  TTCGATGTTG  GCAGCATTTT  CAGACGGCAC  GTCTGCGCCA  GCTGCCTTAC
101 AAACATGGAT  TTTGCGTTCG  GTCAAACGGC  TCAATACCAA  CAGGCCCGGT
151 TTGAAATCCT  CGCGGGCTTC  TTTGATAATG  ACCGTAGGGT  CGGCAGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GGCGAACGGC  TCGGCATCGA
251 CGGCAGGAAT  TTTGCTGAAC  GGACGGGTGC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GGTTCGGGCG  CACTTCTTCG  CCGCTTAAGT  TTGCCAGCGC
351 TTCAGGTGCG  TAG
```

m628.pep

1	MCVPLKPAGC	GPPNSCVSML	AAFSDGTSAP	AAQTWILRS	VKRLNTNRP
51	LKSSAASLIM	TVGSAASGLV	SIALTKMANG	SASTAGILLN	GRVRSVHKP
101	DWIRLRTSS	PLKFASASGA	*		

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLA	AFSDGTSAPAALQ	TWILRSVKRLNTNR	PRLKSSAAS	LIM	
g628	MCVPLKPAGCGPPNSCVSILA	AFSDGTSAPAALHT	WILRSVRR	LNTNR	PRLKSSAAS	LMM
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALT	KMANGSASTAGILL	NGRVRS	SAVHKPDWIR	LRTSSPLKF	ASASGA
g628	TVGSAASGLVSIALT	KMANGSASTAGILL	NGRVRS	SAVHKPDXIR	LRTFSLNF	ASASGT
	70	80	90	100	110	120

q628 X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

```

a628.seq
1   ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT
51  TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
101 ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT
151 CTGAAATCCT CGGCGGCTTC TTTGATCACA ACCACAGGGT CTGCCGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACGC
351 TTCGGGCGCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
1   MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALHTWILRS VKRLNTSKPR
51  LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP
101 DWIRLRTSS PLKFANASGA *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	SDGTSAPAAALQ	TWILRSVKRLN	TNRPLKSSA	ASLIM	
a628	MCVPLKPAGCGPPNSCVSMLAAFS	SDGTSAPAAALHTWILRSVKRLN	TSKPRLKSSA	ASLIT		
	10	20	30	40	50	60
m628.pep	TVGSAASGLVSI	ALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRL	RRTSSPLKFASASGA		
a628	TTGSAASGLVSI	ALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRL	RRTSSPLKFANASGA		
	70	80	90	100	110	120

m628.pep	X
a628	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
1   ATGACTGcca aacCTTTTTC CCTCAACCTG GCcaaCCTCC TGCTGCCggc
51  ggtatTGTTT GCCGTcAGcc tGtcgTcGG cattgccgaT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGcgaT TGTGTGACG GGCgcgtcga tagcgGtggc
201 gGGGAtgatt atgcagATTC TGATGCGCAA CcgtTTTGTC GAGCCTteta
251 tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgcttct gAtgtccctg
301 ctgctgcctg CcgcGccgct gccggtcaAA ATGTCGGtag Ccgccgttgc
351 CGCGCTGATC GGGATGTTGG tctTtatgct gctaataccgC Cgcctgccac
401 cgacggcgca gctgatgGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG
451 GttgaGGCGG TGGCGACGTT TGTCGCGTAT GAGTTTGAGA TGCTGCAAAT
501 GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT
551 ACGAGCTGCT TTGGATTACG GGCGGTTTGG CGGTGTGTTGC CTACCTGATT
601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAGACGGTGA GCGTGAATTT
651 GGGTTTGAAC CGGACGGCGG TGTGTGTTGC GGGTTTGATT ATTGTGGCAC
701 TGATTACATC GCTGGTCATT GTAACGTCG GCAATATTC GTTTATCGGG
751 CTGGTCGTGC CGAATATCGT CAGCCGCCTG ATGGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTCGCCC TCTTGGCGC GTCTTTGTTT TTATTGTGCG
851 ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATTC GGTCTCCACG
901 GTTTTGGTG TGTTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
951 ACCCGCTAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
1   MTAKPFSLNL ANLLLPAVLf AVSLSVGIAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGXIFGGV

```

1005

151 VEAVATTFVAY EFEMQLMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

```
m629.seq
1  ATGACTGCCA AACCTTTTTT CCTCAACCTG ACCAACCTGC TGCTGCTGGC
51  GGTGTTGTTT GCGCTCAGCC TGTCGGTGGG CGTGCCCGAT TTCGCTAGGT
101 CTGATGTGTT TTCACTGTCC GAGACCCAGC AGGTCATGTT CATCCAGCCG
151 CTGCCGCGCA CGTTTGCAT TGTCGTGACG GGC GCGTCGA TGGCGGTGGC
201 CGGCATGATT ATGCAGATT TGATGCGCAA CCGTTTTGTC GAACCGTCGA
251 TGGTGGGGCG ATGACCAAAG CCGCGCTTAG GTTTGCTGCT GATGACCCGT
301 CTGCTGCGCG CCGCGCCGCT GCGGCGAAAA ATGTCGGTTG CGCCGCTTGC
351 CGCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
401 CGACCGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGCGCGTGTG
451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAAAGCAA TGCTGCAAAAT
501 GCTCGCGCTG TGGACAGCAG GCGATTTTTT GAAACGTGCT TGCTGGCGCGT
551 ACGAGCTGCT TTGGATTACG GCGCGTTTGG CGGTGTTTGC CTATCTGATT
601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGTTAA GCGTGAAATT
651 GGGTTTGAAC CGGACGGCGG TGTGTGGTTC GGGTTTGATT ATTGTGCTTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG CCAATATTCG GTTTATCGGG
751 CTGGTCTGTC CGAACATCAT CAGCCGCTGC ATGGGCGACA GGTGCGCCCA
801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG
851 ACATTTATCG ACAGCGTATT GTGTTCCGT TTGAAATTCG GGTCTCTACG
901 GTTTTGGTG TATTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
951 ACCCGCTCAT GCCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

```
m629.pep
1  MTAKPFSNLN  TNLLLLAVLF  AVSLSVGVAD  FRWSDVFSLS  DSQQVMFISR
51  LPRTFAIVLT  GASMAVAGMI  QMILMRNRFV  EPSMVGASQS  AALGQLLMTL
101 LLPAAPLPAPK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIIFGGV
151 IEAVATFIAY ENEMLOMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSNRLQSL RTAVLWSGLI IVALITSLVI VTVGNIFFIG
251 VVVPIIISRL MGDRLRQSLP AVALLGASLV LLCDIIGRVI VFFFEIPVST
301 VFVGLGTALF LWLLLRKPAY AV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	:	:	:	:	:	:
g629	MTAKPFSLNLANLLLPVLFVAVSLSVGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLPAPLPKMSVAAVAALI					
	:	:	:	:	:	:
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLPAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m629.pep	GMLVFMILLIRRLPPTAQLMVPLVGIIFFGGVIEAVATFIAIYENEMQLMGVWQOGDFSSVL					
	:	:	:	:	:	:
g629	GMLVFMILLIRRLPPTAQLMVPLVGXIFFGGVVEAVATFVAYEFEMQLMGVWQOGDFSSVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	:	:	:	:	:	:

1006

```

g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240
           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVFNIIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVFNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300
           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51 GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGGCAT TGTGTTGACG GGCGCGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTG TGATGCGTAA CCGTTTGTG CAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTGCTTCT GATGTCCCTG
301 CTGCTGCCTG CCGCGCCGCT GCGGTCAAA ATGTCGGTGT CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTTTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CTTTGGTTCG GGATTATTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTCGGACGGT
551 ATGAACGTGT GTGGGCAACG GGGATTTTGG CTTTGTTTGC CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA CCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATGTGGCTT
701 TGATTACGTC GCTGTTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGCG TATTGGGTAC GCGTTGTTT TTATGGCTT TGTTAAGGAA
951 ACCTGCTCAT GCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSLNL TNLLLLAVLF AVLSVGVAD FRWSDVFSLS DSQQVMFISR
51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMMLIR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMQLMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVFNIIISRL IGDRLRQSLP AVALLGASLV LLCIDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

m629/a629  95.7% identity in 322 aa overlap

           10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSLNLTNLLLLAVLFAVLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           10      20      30      40      50      60
           70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLLPAPLPKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLLPAPLPVKMSVAAVAALI
           70      80      90      100     110     120
           130     140     150     160     170     180
m629.pep  GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMQLMLGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1007

```

a629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAYENMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATT  TGGTGTGGCT  ggctttgttt  ccccccattgt  tttacggcat
51  gtacaacgtc  GGCGCACAGG  CATTTCGGTGC  CTTAACGCCC  Gatttgcgtgc
101 aacaaagcat  cgcccacgac  ggcaattacg  ccctcgccaa  cgctttgggc
151 atcaatatgt  ccccgaaGc  gggcgtgtTg  ggcaaaatgc  tgttcgGCGC
201 GATttacttc  ctgccgattt  acgcgaccgt  aTTTATTGTG  GGcggcttct
251 ggGaaagtCTT  GTTCGCATC  gtACGCAAAC  ACGAAATCAA  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCCGCCCA  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAA  AACTTCATGA  ACCCTGCGCT  GGCAGGCCGC
451 GCCTTCCTGT  TCTTCGCCTA  CCCCGCCAAC  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAC  CGCGCTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCC  GGCTCCATCG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTTT  GCCCGCATCG
701 CTtcttgGCG  CATTATTGCC  ggCGTGATGA  TCGGTatGat  tGcgatgtCT
751 tcgctgatta  acttcatCGg  ttctgacacc  aaagctatgt  ttgctatgca
801 cttggtacat  ggcacttggt  GGAaagatGa  ttAtcactca  ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pop
1  MMILVWLALF  PPMFYGMYNV  GAQAFGALTP  DLLQOSIAHD  GNYALANALG
51  INMSPEAGVL  GKMLFGAIYF  LPIYATVFIV  GGFWEVLFPAS  VRKHEINEGE
101 FVTSILFALI  VPPTLPLWQA  ALGISFGVVV  AKEVFGGTGK  NFMNPALAGR
151 AFLFFAYPAN  LSGDAVWTAV  DGYSGATALA  QWAHAGADGL  KNAVGTOTIT
201 WMDAFIGKLP  GSIGEVSTLA  LLIGGAFIVE  ARIASWRIIA  GVMIGMIAMS
251 SLINFIGSDT  KAMFAMHLVH  GTWWKDDYHS  LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATT  TGGTGTGGCT  GGCTTTGTTC  CCTGCCATGT  TCTACGGTAT
51  GTACAACGTC  GGCGCGCAGG  CATTTCGGTGC  GTTAACGCCT  GATTTGCTGC
101 AACAAAACAT  CGCCAACGAC  TGGCATTACG  CCTTTGCCAA  CGCTTTGGGC
151 ATCAATATGT  CGTCTGAAGC  GGGCGTGTCG  GACAAAATGC  TGTTTGCGCG
201 GATTTACTTC  CTGCCGATT  ACGCGACTGT  ATTTGTTGTG  GGCGGTTTCT
251 GGGAAAGTTT  GTTCGCCACC  GTGCGCAAAC  ACGAAATCAA  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCCGCCCA  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAA  AACTTCATGA  ACCCTGCGCT  GGCAGGCCGT
451 GCTTTCCTGT  TCTTCGCCTA  CCCTGCCAAC  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAC  CGCACTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCC  GGCTCCATTG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTTT  GCCCGCATCG
701 CTTCTTGCGG  CATTATTGCC  GCGGTGATGA  TCGGTATGAT  TGCGATGTCT
751 TCGCTGTTCA  ACTTCATCGG  TTCGGACACC  AACGCTATGT  TTGCTATGCC

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1008

801 TTGGTACTGG CACTTGGTGG TCGGGGGCTT CGCCATCGGT ATGCTGTTTA
 851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
 901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
 951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
 1001 CCCGATTTC CGACTATTTC GTCGCACAG CGAACATCAA ACGCAGAAAG
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep
 1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG
 51 INMSSEAGVS DKMLFGAIYF LPIYATVFV VGGFWEVL FAT VRKHEINEGF
 101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMN PALAGR
 151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAV TGQTIT
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
 251 SLFNFIGSDT NAMFAMPWYH HLVGGFAG MLFMATDPVS ASFTNVGKWW
 301 YGALIGVMCV LIRVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
 351 ARSNG*

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS					
g630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQSIANDGNYALANALGINMSPEAGVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYFLPIYATVFVGGFWEVL FAT VRKHEINEGFFVTSILFALIVPPTLPLWQA					
g630	GKMLFGAIYFLPIYATVFIVGGFWEVL FASVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVV AKEVFGGTGKNFMN PALAGRAFLFFAYPAN LSGDAVWTAV DGYSGATALA					
g630	ALGISFGVVV AKEVFGGTGKNFMN PALAGRAFLFFAYPAN LSGDAVWTAV DGYSGATALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGLKNAV TGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
g630	QWAAHGADGLKNAV TGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYHHLVGGFAGMLFMATDPVSASFTNVGKWW					
g630	GVMIGMIAMSSLINFIGSDTKAMFAM----HLVHGTWKKDDYHSLYIK.					
	250	260	270	280		
	310	320	330	340	350	
m630.pep	YGALIGVMCVLIRVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq
 1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GGGCGACAGG CATTGCGTGC GTTAACGCCC GATTGTGCTGC
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGCAAAATGC TGTTCCGCGC
 201 GATTACTTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
 251 GGGAAAGTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
 351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
 401 TATTCGGCGG TACAGGTAAG AACTTCATGA ACCCTGCGCT GGCAGGCCGT
 451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
 501 GACGCGGTT GACGGCTATT CCGCGCAAC CGCGCTGGCG CAATGGCGCG
 551 CACACGGTGC AGACGGCCTG AAAACGCCA TAACCGGTCA AACCATCACT
 601 TGGATGGATG CGTTTATCGG CAACTGCCC GGCTCCATCG GCGAAGTCTC
 651 CACTTTGGCA CTCTTAATCG GCGCGCGT TATCGTGTTC GCCCGCATCG

1009

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGTTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTTCC GCTTCCTTCA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPFALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIAN	WHYAFANALGINMSSEAGVS				
a630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQOSIAND	WHYALANALGINMSSEAGVL				
	10	20	30	40	50	60
m630.pep	DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEG	FFVTSILFALIVPPTLPLWQA				
a630	GKMLFGAIYFLPIYATVFIVGGGFWEVLFATVRKHEINEG	FFVTSILFALIVPPTLPLWQA				
	70	80	90	100	110	120
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPFALAGRAFLFFAYPAN	LSGDAVWTAVDGYSGATALA				
a630	ALGISFGVVVAKEVFGGTGKNFMNPFALAGRAFLFFAYPAN	LSGDAVWTAVDGYSGATALA				
	130	140	150	160	170	180
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
	190	200	210	220	230	240
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIG	MLFMDPVSASFTNVGKWW				
a630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIG	MLFMDPVSASFTNVGKWW				
	250	260	270	280	290	300
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
a630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTGCGAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATCGCGCG CATATCCTCA AACGACGCGC
201 GCATCTGTTT CTTACCCAGT TTTTCCAACA CTCTCTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAG

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301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCGCCGCG GCTTTCCAAC
351 TCTGCAATTG GATTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

g635.pap

1 MTRRRVGKQN RIAIHSQYR KMOVFAVFI HDDGDFQLRE LFERQGIAGR
51 LKTQIGHNAP HILKRAHLF LTQFFQHFFF RQLLPVKIVQ KRRHRSRPAG
101 KIOILLYNIE IPPREPTLOF DFSVNNRIIV KHRCSTOTIR QGSVPD*

m635.seq

1	ATGACCCAGC	GACGGGTCGG	CAAGCAAAAC	CGTATTGCGC	TCTATACCGC
51	CGAATACGCA	GAATATGATCA	TCTTTCGGGT	ATTTCAGATA	CACGATGACG
101	GGGATTTCGA	ACTGTGCAAG	CTCGTCGAAA	GACAGGGCAT	AGCCTTTCGC
151	TTCAAAACCC	AAATCAGGCA	TAATTCGCGC	CGATCTCTCA	AACACGCGGG
201	GCATCTGCTC	CTTATCCAGT	TTTTTTAAAC	CGCTCTTTC	CGTCAGCTTT
251	TGCCCGTAAA	AATGTGTTCA	AAGCGTCAAC	ACCGAAGCCG	CCCCGAGGGA
301	AAAATCAAAA	TCTGTGTTTA	CAATTAATGA	ATCGCGCTTT	TCTTTCCAAC
351	TCTGCAGCTT	TGTTTTTCCA	GAAGCAACAG	GATTATATGT	GATTAA

m635.pcp

1 MTQRRVGKQN RIAVYTAQYR EMILAVFOI HDDGDLQLCK LLERQGIAFR
51 FKQTQIRHNP HILKRRGHLL LIQFF*HVLV RQLLPVKIVQ KRHHRSRPAG
101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/q635 80.0% identity in 130 aa overlap

		10	20	30	40	50	60
m635.pep		MTQRRVVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP					
		:: ::: ::: ::				::: ::	
g635		MTRRRVVGKQNRIAIHSAQYRKMMVVFAVFQIHDDGDFQLRELFERQGIARLKTQIGHNAP					
		10	20	30	40	50	60
		70	80	90	100	110	120
m635.pep		HILKRGRHLLLIQFFXHVLFQRLLPVKIVQKRHRHSRPAGKIQILLYNIEIAPFPPTLHF					
		:: :	:	:	:		:
g635		HILKRRAHLFTQFFQHFFFRQLLPVKIVQKRHRHSRPAGKIQILLYNIEIPPRPPTLQF					
		70	80	90	100	110	120
		130					
m635.pep		DFSISNRRIIVDX					
		::					
g635		DFSVNNRRIIVKHRCISIQTIRQGSVPDX					
		130	140				

a635.seq

1	ATGACCCAGC	GACGGGTCGG	CAAGCAAAAC	CGTATTGCCG	TCTATACCGC
51	GCAATATCCGA	GAATATGATCA	TCCTTGCGGT	ATTTCAGATA	CACGATAGCG
101	GGGATTTGCCA	ACTGTGCAAG	CTGCTCGAA	GACAGGCGAT	AGCCTTTCCG
151	CTCAAAACCC	AAATCAGGCA	TGATGCGCCG	CATATCCCTA	AACGACGCGC
201	GCATCTGCTC	CTTATCCAGC	TTTTTCAACA	CGTCCTCTTC	CGTCAGCTTT
251	TGCCCGTGAA	AATTTGTTCAA	AAGCGCTCGC	ACCGAAGCGT	CCCTCGAGGA
301	AAAATCCAAA	TCTTGCTTTA	CAATATTTGAA	ATCGCGCCTT	TCTTTCCAAC
351	TCGTCACTTT	GATTTTTCCTA	TAAGCAACAG	GATTATAGTG	GATTAA

a635.per

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAGR
51 LKTQIRHDAP HILKRRRAHLL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
101 KIOILLYNIE IAPFFPTLHF DESISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10 20 30 40 50 60

1011

```

m635.pep    MTQRRVKGQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP
a635        MTQRRVKGQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHDA
              10      20      30      40      50      60

              70      80      90      100     110     120
m635.pep    HILKRRGHLLLIQFFXHVLFRLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
a635        HILKRRGHLLLIQFFXHVLFRLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
              70      80      90      100     110     120

              130
m635.pep    DFSISNRIIVDX
a635        DFSISNRIIVDX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTAT TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcccgg CgcgtTCCAA ACGGTAACGC CATTGCCCGG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GGCGCGGGCA AAAATTTTCG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCAGC
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCGGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCTGTGTTT
951 TATACGCAAA CCGCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGKNVVPFPG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIIVFNQG ARGGFFEINT GIHCWQAHNT TGNGQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACACG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTAT TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCCGG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTGC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

1012

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep
 1 MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVIH VDGETQIAEA VVFIGVVRAG
 101 IGKNAVPPFG NVVADDLRTG CVPNGNAVA LVHAQSRVAD DFILAHHRIG
 151 RTMQIYADRI IQNIVVFNQG ARGSFEEINT GIHCGQAHTG TGNGQVAERY
 201 VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
 251 GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVG	IIGKYALACL	VDNVVNIGI	VDIVEHNALI	AAADGDIVEY	FEPLGKHQHI
g638	MIGGQFIVVG	IVGKNALARF	VDNVVNIGI	VDIVEHDALI	AAADGDIVEH	FEPFGKHQHI
	10	20	30	40	50	60
	70	80	90	100	110	120
m638.pep	AHIVAHGNIA	ADFAVVGVIH	VDGETQIAEA	VVFIGVVRAG	IGKNAVPPFG	NVVADDLRTG
g638	AHIVAHGNIA	ADFAVVGVIH	VDGETQVAEA	VVFIGVVRAG	IGKNAVPPFG	NVVADDLRAG
	70	80	90	100	110	120
	130	140	150	160	170	180
m638.pep	CVPNGNAVA	LVHAQSRVAD	DFILAHHRIG	RTMQIYADRI	IQNIVVFNQG	ARGSFEEINT
g638	RVPNGNAIA	ALHAQGR	IADDFILAHHRIG	RTMKVYAE	RIKNI	VVFNQARGGFEINT
	130	140	150	160	170	180
	190	200	210	220	230	240
m638.pep	GIHCGQAHTG	TGNGQVAERY	VRRVYGYGTP	PAPVAFDGCCT	VGRPFNRNRF	VNVKFGFIYA
g638	GIHCWQAHTG	TGNGQVAERY	VRRVYGYGTP	PALVPFDGCCT	VGRPFNRNRF	VDIKFGLIYA
	190	200	210	220	230	240
	250	260				
m638.pep	GSQFERIARP	GAGKCGIPIS	IIGSX			
g638	GSQFDRIARP	GAGKCNFGK	VVLRGNVDDG	CRCLKNAAG	GKYQHGLQ	PYTERGCVH
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq
 1 ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
 51 TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
 101 TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
 151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
 201 AAATATTGCC GCTGATTTTC CTGTCGTTGG TGTACATATA GTGGACGGCG
 251 AAACGCAAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
 301 ATTGGAAGAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
 351 GCGCGCCGGG CGCGTTCCTA ACGGTAACGC CATTGCCGCG CTCGTTACAG
 401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
 451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
 501 CAATCAGGGC GCGCGGGGCA GTTCTTCTGA GATAAATACC GGCATCCATT
 551 GCGGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
 601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
 651 TTGCAGAAGC GTCGCGAGGC CTTCAATCG TAATCGGTTT GTCGATGTGA
 701 AGTTTGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
 751 GCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep
 1 MIGGQFIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVIH VDGETQIAEA VVFIGVVRAG
 101 IGKNAVPPFG NIVADDLRAG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
 151 RTMQIDADRI IQNIIVFNQG ARGSFEEINT GIHCGQAHTG TGNGQVAERY
 201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGLIYA GSQFERIARP

1013

251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLDVNVVNVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI					
a638	MIGGQFIVVGIVGKNALARFVDNVVNVNIGIVDIVEHDALVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADFVVGHVHVDGETQIAEAVVFGVVRAGIGKNAVPPFGNVVADDLRTG					
a638	AHIVAHGNIAADFVVGHVHVDGETQIAEAVVFIGVVRAGIGKNAVPPFGNIVADDLRTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m638.pep	CVPNGNAVALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIIVFNQGARGSFEEINT					
a638	RVPNGNAIALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQGARGSFEEINT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGCRTVGRPFNRNRFVDVKFGLIYA					
	190	200	210	220	230	240
	250	260				
m638.pep	GSQFERIARPGAGKCGIPISIIGSX					
a638	GSQFERIARPGAGKCGIPISIIDSX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAAAC CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTAGTA CGCGCTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGGCAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEVSGN ISVGNMGGYV LMFSERLKVF DNIAVGSRD*
151 GIMLNIVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLDHN SFINNGSQVK YVSTRFLDWS EGGHGNYSW NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEAET ROSEGRGAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1   ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTCCCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCGGT GCGCAGGTGC TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACT CCTACAAAAA CAACCGCTTC
301 AGCGATTGTC GTTTCGCGCT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCG GATATTCACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCTTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAA TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTACGCA CGCGCTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGGCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC CAGGCGCAG TTTCCGCGC TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAACG CGGCAGTCGG
1001 AATGGGCGAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1   MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNST THNTYKNNRF
101 SDLRFVHYM YTNDSSEISG ISVGNMGGYV LMFSERLKVF DNIIVGSRDQ
151 GIMLNYYVNS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLDHN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKET RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWVAPGAQVVGNDISKGRDGIFSNSTTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWVAPGAQVVGNDISKGRDGIFSNSTTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMGGYVLMFSERLKVF DNIIVGSRDXGIMLNYYVNSDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGGYVLMFSERLKVF DNIIVGSRDQIMLNYYVNSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTA AIEGTSLDHNSFINNGSQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSGDSAYRPDGIIDQIIWRAPVSRLLMNSPAISIVKWAQAF FPAVLPGGVV					
m639-1	NSAFDLNGDGFSGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAF FPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLEKETRQSEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLEKETRQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

1015

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGCCTC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 GCGCGCCGGC GCGCAGGTCG TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAAG ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTC GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAAGCG GGCAAGTGGC TTTTTCCTTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTCAGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAA TTTCCGCGC TTTTGCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCGGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGCGAG GCGGAAAAC GTTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNPAG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNMNGYV LMFSERLKVF DNIAVGSRDQ
151 GIMLNVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLDHN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNQ IIDQIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a639-1.pep	NGVTVWNPAGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWNPAGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a639-1.pep	ISVGNMNGYVLMFSERLKVFDNIAVGSRDQGIMLNVNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMNGYVLMFSERLKVFDNIAVGSRDQGIMLNVNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a639-1.pep	YDKLSANHFENCQIGIHFTAIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a639-1.pep	NSAFDLNGDGFSDSAYRPNQIIDQIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDSAYRPNQIIDQIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
	310	320	330	340		
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

1016

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCAGC
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTGTA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
501 GCGCGCCGGC GACATCATCA GcggTGCgAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTGCGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCAGC CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTGTGA TGTTCCTTG GTCCAGCAGC CTTCATCGG TAAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCAGAGCTGC
1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAAGT TTCTTGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTGACGGT GCGGAGCCGT GCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNSIQRS YKVIANQYRL
201 GSDKALQTAS ASDVREAPA SETPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGD PD FIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGYVRGGI FDRIEMIQE
351 NSFRFTDAQH ERVELSAAD APREKESWF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCAGC
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1  MIHIISILKS IGISGIVMSC FSIKMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK					
	: : : : :					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

1017

```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMVLAN
                ||||||||||||||||||||||||||||||||||||||||||||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMALAN
                70      80      90      100     110     120

                130     140
m640.pep      DGTIAGAKLV DHHEPIMLIGIPH
                ||||||||||||||||
g640          DGTIAGAKLV DHHEPIMLIGIPQSRVDKFIDKYIGLNFIFKNPPTPSVAPGDIISGATVTL
                130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
  1  ATGATTTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
 51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101  CCGCGTTTT TGCCTGCTT GTCTTTTGA CCGCGGCACT GCCCGCTTAT
151  GCGGAGCGTC TGCCTGATT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201  TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCC
251  GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301  GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGC
351  GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGT GATCACCATG
401  AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
  1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
 51  AERLPDFLAK IQPSEIVPGA DRYSKPEGK MVARVYKGDE QLGLVYITTD
101  AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

                10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFELTAALPAYAERLPDFLAK
                ||||||||||||||||||||||||||||||||||||||||||||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFELTAALPAYAERLPDFLAK
                10      20      30      40      50      60

                70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMVLAN
                ||||| |||||:|||||||||||||||||||||||||||||||:|:
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITDDAVNTRGYSSKPIDTLMALAK
                70      80      90      100     110     120

                130     140
m640.pep      DGTIAGAKLV DHHEPIMLIGIPH
                ||||||||||||
a640          DGTIAGAKLV DHHEPIMLIGIPH
                130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
  1  ATGCGGTATC CGCCGCAATC GCGGTTTTG CAGAATGCCG CGCGTTGCCT
 51  TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101  TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151  GGTGTCTTCG GTTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201  TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTC
251  TGCAGGAAGC TCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301  GGcaaagcgg ACatcggtTT Gcacggcgtc gagCAGGGtt tgggtTTTTGT
351  CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAACTGG
401  TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451  GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAC
501  CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGGCGgc gTAAGTGAT
551  TCCGTGGCGa ggGTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601  ggGCGgcgac ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTTCG
651  AAACCTGATG GCGGCGTTGG ATTCGCGGC GTTCGTAATC GACGAATCTG

```


1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAAGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAAGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGCGAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTTCGCGGC
1051 GttgACGTAA ATGGTttgtt cgtcgggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAT cgCcgcgccg .gaggtTtcgg gttcggtaAc gccccaaacgg
1151 cggcttttcgc ctTTGAAAAA CATGTCCAAA CCTTGTGCGA CTTGCGcttc
1201 gccgcccgaac tCTTGCAAG GCTGCAACAC CAGCGCGCCT TCGATGCGCG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

```

g642.pep
1 MRYPPQSAVL QNAARCLLRR PKSACRRICP LSAISAVQYI FADVVOQEGC
51 GVVFVFLLYED KKS GDDFADE DFLQAGVVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFLVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WWSAFKTLRA QEFLLHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFNH
251 AVRHADQLQA AADKDVLERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQOV DDFGEFAVFA LFGGNEEVA LRIALPVFRG
351 VDVGLEFVGI FVAGLHFACN RRAGGFGFGN AQTAFAFEN HVQTLCDLRF
401 AEELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

```

m642.seq (partial)
1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGCCGAT GTCGTTCAGC AGGAAGGCTG CGGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTC
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTT CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGATGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TCGCGGCGCG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTGCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCGCG
601 GATTTGCGCG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTGCAGGC ATTTCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTGGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTTGAAAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

```

m642.pep (partial)
1 ACRRICPLPA ISAVQYIFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVSFQI FKDVFNHNAVR HADQLQAAAD KDVLERAGTG
251 SVALGEFHNG GCRHFGIDAV DGVTGGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVFAFALFV GNEEEVALRV ALPVFRGVDV NGLSVDIFVV GLHFACNRRR
351 GGFGFGNTQT AALAFENHLQ TLRDLRFIAE LLQLLQHORA FDAGTQRNGH
401 AVMPRNP

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VVQEGCGVFVFR	LYED	
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VVQEGCGVFVFL	LYED				
	10	20	30	40	50	60	
m642.pep	40	50	60	70	80	90	
	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH					
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFRQSVVAGNGGKADIGLHGVEQGLV	FVQLN					
	70	80	90	100	110	120	
m642.pep	100	110	120	130	140	150	
	ACFFFFGGGADKLVNFGIKHIVRAFKNREGADVDS	DIAGGVSAFKTLRTQEF	LQHLRGG				
g642	ACFFFFGGGADELNVNFGIKHIVRAFKNREGADIDGDIAGWVSAFKTLRLAQEF	LQHLRGG					
	130	140	150	160	170	180	
m642.pep	160	170	180	190	200	210	
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVK	NLGNLMAAPDFAAFVIDE	FDDVVDVS				
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVK	DFGNLMAALDFAAFVIDES	DIVADIS				
	190	200	210	220	230	240	
m642.pep	220	230	240	250	260	270	
	FQIFKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVALGEFHHGGCRHFGIDAVD	GVTGDA				
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVAPGEFHHGGCRHFGIDAVD	GVTGDA				
	250	260	270	280	290	300	
m642.pep	280	290	300	310	320	330	
	QAFGCEGFADVCFGDEQQVDDFGEFAVFALF	GGNEEEVALRVLPVFRGVDV	NGLSVDI				
g642	QAFGCEGFADVCFGDEQQVDDFGEFAVFALF	GGNEEEVALRIALPVFRGVDV	NGLFVGI				
	310	320	330	340	350	360	
m642.pep	340	350	360	370	380	390	
	FVVGHLHFACNRRAGGFGFGNTQTAALAFENH	LQTLRDLRFIAELLQWLQHQRAFDAGTQR					
g642	FVAGLHFACNRRAGGFGFGNAQTAAFAFENH	VQTLCDLRFIAELLQRLQHQRAFDAGTQR					
	370	380	390	400	410	420	
m642.pep	400						
	NGHAVMPRNP						
g642	NGHAVMPRNPX						
	430						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCC GCTATCCGCA ATATCGGCAG TCCAATATGT
51 CTTTGCGGAT GTCGTTTCAGC AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GCGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTT CTGCAGGAAG CTGCGGATGT
201 CTTCGGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGTT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGCAGCGCGG CGTAAGTGT TCCGTGGCG AGGGTTTGA
501 CGATGTTTCG TCATCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCAGCGCCG
601 GATTTCCGCG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCATAA TGCCGTGCGT CATGCCGATC

```

1020

```

701 AGTTGCAGGC GGCTGCCGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGGC ATTTCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCCGGG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVFSQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHG GCRHFGIDAV DGVT DGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFV RLHFSGNRRA
351 GGFGFNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

m642.pep      10      20      30      40      50      60
ACRRICPLSAISAVQYIFADVQEGCGVFVFRLYEDKESGDDFADKDFLQAGAGIGQGVF
|||||
a642          10      20      30      40      50      60
ACRRICPLSAISAVQYVFADVQEGCGVFVFRLYEDKESGDDFADKDFLQAGAGIGQGVF
|||||

m642.pep      70      80      90      100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLNVNFGIKHIV
|||||
a642          70      80      90      100     110     120
LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLNVNFGIKHIV
|||||

m642.pep     130     140     150     160     170     180
RAFKNREGADVDSDIAGGVSAFKTLRQEFQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
|||||
a642         130     140     150     160     170     180
RAFKNREGADVDSDIAGGVSAFKTLRAQEFQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
|||||

m642.pep     190     200     210     220     230     240
RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVFSQIFKDVFNHNAVRHADQLQAAAD
|||||
a642         190     200     210     220     230     240
GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVFSQVFKGVFNHNAVRHADQLQAAAD
|||||

m642.pep     250     260     270     280     290     300
KDVLERAQTG SVALGEFHGGCRHFGIDAVDGVT DGAQAFGCEGFAADVC FGDEQQVDDF
|||||
a642         250     260     270     280     290     300
KDVLERAQTG SVALGEFHGGCRHFGIDAVDGVT DGAQAFGCEGFAADVC FGDEQQVDDF
|||||

m642.pep     310     320     330     340     350     360
GEFAVAFALFGGNEEEVALRV ALPVFRGVDV NGLSVDIFVVG LHFACNRRAGGFGFGNTQT
|||||
a642         310     320     330     340     350     360
GEFAVAFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFVVR LHFSGNRRAGGFGFGNAXT
|||||

m642.pep     370     380     390     400
AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
|||||
a642         370     380     390     400
AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
|||||

```

1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

g643.seq

```

1 ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
51 gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTCCAAACG TGCCCGCGT TtgCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagatGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGat
351 GACCTGCGCg aGTGtTCCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTg a

```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

g643.pep

```

1 MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
51 ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPM TAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGGMTCA SVAVW VSDGM AVCFSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

m643.seq

```

1 ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTCCAAACG TACCCGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTg A

```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

m643.pep

```

1 MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
51 ATRVSKRTRR LPSAAVCCG DAEILCSATV SGVPM TAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVW VSDGM AVCFSV*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*.

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
g643	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPM TAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
g643	LPSAATVCCGDEEMLCSATVSGVPM TAEMVSSACRRRLFRATSCMSSSAAACMSFGGMTCA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMAVCFSVX					
g643	SVAVWVSDGMAVCFSVX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

a643.seq
 1 ATGGTGTTGC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
 51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
 101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTGCCCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
 201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
 351 GATCTGCGCG AGTGTTCGGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
 401 TTTCGGTTTG A

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

a643.pep
 1 MVLPLMLLAT IRSATLTL*L LAMLN RVSPS TTRWMLAWSG EISASPSAAL
 51 ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFSV*

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAAL	ATR VSKRTRR				
a643	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAAL	ATR VSKRTRR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAA	CMSFWGMICA				
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAA	CMSFWGTICA				
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGM	AVCF SVX				
a643	SVAVWVSDGM	AVCF SVX				
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

g644.seq
 1 ATGCGCTCTG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
 51 GTTTAGAAAA TTAACCTAA ACTGTGGCAG CGGCTTTGAC CGGCCGCGGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAaagcaca tcgaatCCGC
 201 ATTcCCCCGC ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAG ACGGCGGGCG CAAGGCGAGT CAGTTTGAAT TCCAAGAAGT
 351 CCTAAGGATT GCGGGGCATT ACGCGGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCTCTGC AAGagttcgg cggcgaagcG
 451 CAAGTCGCAC AAGGTTTGA CATGATTTC AAaggcgaaa gccgcggttt
 501 gggcgTtacc gaaccggaAa cctccggcgc gGgaATTGCA CGCGAAAtgc
 551 agtcctgcta cgaatatacc gacgaacaAA CCATTACGT caaCGCCGCG
 601 AAATACTGGC AGGGCAATTG GCAAAGCGAC TTCTcctcg ttgcccgcga
 651 agagcgcaaa aacGGcaaac tcgccaaagt CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CCTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
 801 GATGAAATC TCCCGGGGCG ACGCTGCCGG TTGCGCGCG TCCAAAACA
 851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
 951 CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCCATCAG GTTTCGAAA
 1001 TCCTTTACCG CTACGTCTGC CATTCCGTTT CGcccgtegc GCccgTCGCC
 1051 CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCCA CGGAATACAC
 1101 TTAacgCGCC GCGCAAATGT TGCAAAACT CTGGGCGCG AAGGGTTTG
 1151 AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACGACCAATT
 1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGACAAAA
 1301 accaaaCCCT Gctcgacgcc gtgCAAaccg atGTCCgctt tgCCGCCGTT
 1351 GCCcgcGacT ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTTGACC GACGCCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

g644.pap

1	MPSPERPADCC	PVHFVVKFRK	LTLCNGRRFD	RPPINGNRQR	KPMIHTEPSA
51	QPSTMDTAAG	LKHIESAFPR	IFSDGIDLMR	YLPEDKWLAL	QKAGLLHFFL
101	DKKHGGKRAE	QEFIGEVLRI	AGHYGVPTLR	RTGIEGALVL	QPLQEGFGEA
151	VQAQGLDMIF	KGESRRLGVT	EPETSGAAIA	REMQSCYEYT	DEQTIYVNAA
201	KYWQGNQSOD	FLLVAAKERK	NGKLAKVIDL	LLVPKTYIRC	ETLASEGLRA
251	VRYAVNSRDA	EMPATAMVKL	SRGEAAGLRA	FQNFIIRSRL	QLIGMTHGIM
301	EYILDNLNRY	VNRNDRFVDY	ERREIQRHRQ	VESEILRYVC	HSVSPVAPVA
351	HQLMEANIVK	TLATEYTYAA	AQMLQKLLGA	KGFERGHYPG	NIAIDIRPFT
401	IFEGPNMDLY	AEIYDQFVRA	TAEKEAGIKI	LDKNQTLTLD	VQTDVRFRAV
451	ARDYALPDRI	RSFLQHEFTL	DACALQKVFV	GKIIARLFVF	VQEEHEDTTA
501	FLLDNRKDID	LDRCYCG*			

m644.seq

1	ATGCCGCTGTG	AAAGGTCGGC	GGATTGTTGC	CCGGCGCACT	TTGTGGTAA
51	GTTTAGAAAA	TCAACTCTAA	ACTGTGGCAG	CGCGTTTGAC	CGCGCCGCCA
101	TTAATTAGAA	CCGACAGAGG	AACCCGATGA	TACATACCGA	ACCCGAGCGG
151	CAGCCGTCAA	CTATGGACAC	GGCTGCTTTT	TTAAAGCACA	TCGAATCCGC
201	ATTCCGCGAG	ATTTTTTCAG	ACGGTATCGA	CCTGATGCGA	TACCTCGCCG
251	AAGACAAATG	GCTTGCCTTG	AAGCAGCGCG	GTTTGCTGTT	GCCCTTCTCT
301	GACAAAAAAT	ACGGCGGGCG	CAGGGCGAGC	CGATTGTA	TTCCAAGAAGT
351	CcTGCGGATT	CGCGGGCATT	ACGGCGTGCC	CGTTACGCTG	CGTACCGGCA
401	TCGAAGCGCG	GCTGGTGTG	CAGCCACTGC	AAGAGTTCCG	CGATGAAGCG
451	CAAGTCGCGC	AAGGTTTGA	GATGATTTC	AAGGCGAGG	CGCGCGGTTT
501	GGGTGTTACC	GAACCCGAAA	CCTCGGGCG	GGCGATTGCA	CGCGAAATGC
551	AGTCTCTACTA	CGAATATATC	GACGAGCAAA	CCATTTACGT	CAACGCCCGC
601	AAATACTGGG	AGGCGCAATC	CAGACGCGAC	TTCTCTCTCG	TTTCGGCGAA
651	AGAGCGCAAA	AACGGCAAAC	TCGCCAAAGT	CATCGACCTG	CTGCTCGTCC
701	CCAAAACATA	CATCCGCTGC	GAAACCCCTG	CATCCGAAGG	CTTGCGCGCC
751	GTCCGTTACG	CCGTCAACCG	CATCGATGCC	GAAATGCGTG	CAACCCCGCT
801	GATGAAACTC	TCCCAGAGCG	ACGCTGCCGG	TTTGCGCGCG	TTCCAAAACA
851	TCTTTATCCG	CAGCCGCGTG	GAACTATGCG	CGATGACGCA	CGGCATTATG
901	GAATATACATC	TGAAAAATCT	GCAACGATAC	GTCCGCAACG	ACATCAAAAT
951	CGTCGATTAC	GAACGCCGCG	AAATCCGGCG	CCGCCATCAG	GTTTCCGAGA
1001	TTCTTTTACG	CTACGTCTGC	CATTCCGTTT	CGCCTGTTTG	CCCGCTGCCG
1051	CATCAGCTGA	TGGAGCGGCA	CATCGTCAAA	ACCCCTGCCA	CGGAATACAC
1101	TTACGCGCGC	TGCGAAATGT	TGCAAAAAC	CTTGGGTGCG	AAGGGTTTTG
1151	AACGCGGACA	CACCGCCGCG	AATATCGCTA	TCGACATCCG	CCCTCTCACG
1201	ATTTTGTGA	GCCCAGACA	TATGCTTTAT	GCGGAAATTT	ACGACCAATT
1251	TGTTCCGCGC	ACGGCCGAAG	AAAAAGAAC	AGCCATGAAG	TTGGAGAAAA
1301	ACCAAACCTT	GCTCGACCGC	CTGCAAAACG	ATGCCCGCTT	TGCCCGCGTC
1351	GCCCGCGACT	ACACTTTGCG	TGAAGACATC	CGCAGCTTTC	TGCAGGAACA
1401	CACCTGACG	GATGCTTGGC	CCCTGCAAAA	AGCTTTTATC	TGC AAAATCA
1451	TGCGCCGACT	CTTTGTCTTC	GTACAGCGCA	AACACGAAGA	CACCGCAGCC
1501	TTCTGTCTGA	ACGACATCCG	CAAAGATATA	TTGGACTGCC	GATATTGCGG
1551	GTAG				

m644.pgp

1	MPSERSADCC	PAHFVVKFRK	STLNCGRFRD	RPPINGNRQR	KPMIHTEPSA
51	QPSTMDTAAF	LKHEISAFRR	IFSDGIDLMR	YLPEDKWLAL	KQAGLLHFPF
101	DKKYQGRKGS	QFIEQEVLR	AGHYGVPTVL	RTGIEGALVL	KQOQEFEGDEA
151	QVAQGLEMF	KGEGGGLGVT	EPETSGAIA	REMQSYEYI	DGQTYIVNAA
201	KYWQGNSQSD	FLLVAAKERK	NGKLAKVIDL	LLVPKTYIRC	ETLASEGLRA
251	VRYAVNRIDA	EMPATAVMKL	SQSDAAGLRA	FQNIIFIRSL	QLIGMTHGIM
301	EYILENLERY	VRNDIKFVDY	ERREIRRHRQ	VEILRYRVC	HSVPVAPVA
351	HQLMEANIVK	TLATEXTYAA	AQMLQKLPGA	KGFERGHTAG	NIADIRPFT
401	IFEGPNDMLY	AEIYDQFVRA	TAEKEAGMK	LDKNQTLDDR	LQTDARFAAV
451	ARDYTLRPDI	RSFLQVETLT	DACALQKVFI	GKIIARLFVF	VQAKHEDTAA
501	FLLNDLRKDI	LDCRYCG*			

10 20 30 40 50 60
 m644.pep MPSERSADCCPAHFVVKFRKSTLNCGRREFDRPPINGNRQRKPMIHTEPSAQPSTMDTAA
 ||||| ||||| ||||| ||||| ||||| |||||
 α644 MPSERPADCCPVHFVVKFRKLTLCGRREFDRPPINGNRQRKPMIHTEPSAQPSTMDTAA

1024

	10	20	30	40	50	60
	70	80	90	100	110	120
m644.pep	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKYGGKSGQFEIQEVLRI					
g644	LKHIESAFPRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKHGGRKSGQFEIQEVLRI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m644.pep	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLEMIKFGEGGGLGVTEPETSGAAIA					
g644	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLDMIKFGESRRGLGVTEPETSGAAIA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m644.pep	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
g644	REMQSCYEYTDQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
	190	200	210	220	230	240
	250	260	270	280	290	300
m644.pep	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m644.pep	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
g644	EYILDNLNRYVRNDIRFVDYERREIQRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m644.pep	TLATEYTYAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
g644	TLATEYTYAAQMLQKLLGAKGFERGHPAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644.pep	TAEKEAGMKLDKNQTLRLQTDARFAAVARDYTLPEDIRSFLQEHILTACALQKVFI					
g644	TAEKEAGIKLDKNQTLRLDAVQTDVRFDAVARDYALPEDIRSFLQEHILTACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644.pep	GKIIARLFVVFQAKHEDTAAFLNDIRKIDILDCRYCGX					
g644	GKIIARLFVVFQEEHEDTAAFLNDIRKIDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

a644.seq

```

1  ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCCTG AAGCAGGCGG GTTGTGCTGT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTTG CAGCCACTGC AAGAGTTCCG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGGA CATGGTTTTT AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTACGT CAACGCCGCG
601 AAATACTGCG AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAACTC TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAACA

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1025

```
851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACCGGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCGCGGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```
a644.pep
1  MPERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAIA REMQSYEYD DGQTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FIRSRL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFV VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*
```

m644/a644 97.3% identity in 517 aa overlap

```
m644.pep      10      20      30      40      50      60
MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
|||||
a644          10      20      30      40      50      60
MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF

m644.pep      70      80      90     100     110     120
LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGRKGSQFEIQEVLRI
|||||
a644          70      80      90     100     110     120
LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGRKGSQFEIQEVLRI

m644.pep     130     140     150     160     170     180
AGHYGVPVTLRTGIEGALVLQPLQEFQDEAQAQGLEMIFKGGGGGLGVTEPETSGAIA
|||||: : |||||: |||||: |||||: |||||
a644         130     140     150     160     170     180
AGHYGVPVXXXXXEGALVLQPLQEFQDEAQIAQGLDMVFKGGGGGLGVTEPETSGAIA

m644.pep     190     200     210     220     230     240
REMQSYEYIDGQTIYVNAAKYWGNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC
|||||
a644         190     200     210     220     230     240
REMQSYEYTDGQTIYVNAAKYWGNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC

m644.pep     250     260     270     280     290     300
ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
|||||
a644         250     260     270     280     290     300
ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM

m644.pep     310     320     330     340     350     360
EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLEMEANIVK
|| |||||: |||||: |||||: |||||: |||||
a644         310     320     330     340     350     360
EYILENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLEMEANIVK
```


1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644						
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLDRLOTDAFVAARDYTLPEDIRSFLQEHTLTDACALQKVFI					
a644						
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
a644						
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATGTCG ATGCCGGTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTTGCTG CAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCAGCG AGTTGTCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAaata CCTGTCCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TCGCGGGAAT CGGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGTCGCACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGCGGAAAC GGTGCGCGAA
651 GTTTTGC GCG TGTGCTCGA CCAGAAGCGT GGTGCGGCGC AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGcgcgcat ggcggcggc TGGTCTTCGG
851 TTTCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

m645 . pep

```

1  MMMVLALGMS MPVSMMEQS NTLNLCKKKS RMTSSSSRSR SCPCATPIRA
51  SGRSVSSRSR IFSIVSTSLC RKNTPPRLS SRNTASRTLP SLNGLTKVFT
101 ARRLGAVVI SEKSRPPSSA MLVRGIGVA VMVRMSTLAR RRLSCSFCRT
151 PKRCSSSIIN KPKFLNFMSS CTNLCPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKAFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTAA ATCGTTGCTG CAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCTGTCCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAAAGCC ATACTTAAAG TACGCGGAAT CGGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGCGGAAAC GGTGCGCGAA
651 GTTTTGC GCG TGTGCTCGA CCAAAAGCGT GGTGCGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTTAATCA CGGCGCGCAT GCGGCGGCC TGGTCTTCGG

```

1027

851 TTTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep
 1 MMVLALGIS IPVSMVEQS NTLNRCKKKS RMTCSSSRSR SCPCATPMRA
 51 SGRVSSSR SR IFSIVSTSLC RKNTCPPLRS SRNTASRTLP SLKGLTKVLT
 101 ARRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
 151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLK
 201 RERLATFTGK SAKRSKAFCA CCSTKSUVGA STATCLPPIT ATNAARRATS
 251 VLPKPTSPHT RRSIGFACVK SLITAMAAA WSSVSS*

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMVLALGISIPVSM	VEQSN	TLNRCKKSRMT	CSSSRSR	SCPCATPMRAS	GRVSSSR
g645	MMVLALGMSMPVSM	VEQSN	TLNRCKKSRMT	CSSSRSR	SCPCATPIRAS	GRVSSSR

	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNT	CPPLSSRN	TASRTLPS	LKGLTKVLT	ARRRLGAV	VISEKSRSP
g645	IFSIVSTSLCRKNT	CPPLSSRN	TASRTLPS	LNGLTQVFT	ARRRLGAV	VISEKSRSP

	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVR	ISTLARRL	SCSFRTPK	RCSIIITK	PKFLNLMSS	CTSLCVPIT
g645	MLVRGIGVAVMVR	ISTLARRL	SCSFRTPK	RCSIIINK	PKFLNFMSS	CTNLCVPIT

	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALV	ALLKRE	RLATFTGK	SAKRSKAF	CACCSTKS	VVGASTATC
g645	STVPSAMPSSVAL	ALLKRE	RLATFTGK	SAKRSKAF	CACCSTRS	VVGASTATC

	250	260	270	280
m645.pep	ATNAARRATSVLP	KPTSPHTR	RSIGFACV	KS
g645	ATNAARRATSVLP	KPTSPHTS	RSIGFACV	KS

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq
 1 ATGATGATGG TGTGGCGTT GGGAAATGTCG ATACCGGTTT CGATGATGGT
 51 GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAGTTCG CGCATGACTT
 101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
 151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
 201 TTCATTGTGC AGGAAAAATA CTGCCC GCCGCTTTGAGT TCGCGCAATA
 251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTTTGACG
 301 GCGAGGCGGC GGCTGGGCGC AGTGGAATC AGCGAGAAGT CGCGCAGTCC
 351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
 401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCAGC
 451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
 501 TATGTCGTCC TGCACCAAGT TGTGCGTACC GATAACAATA TCGACCGTGC
 551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
 601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTGCGCAAA
 651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGTGGC AGTACGGCAA
 701 CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GGCAGACTCG
 751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
 801 CTGCGTCAAA TCTTAATCA CGGCGGCGAT GGCAGCTGCC TGGTCTTCGC
 851 TTTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep
 1 MMVLALGMS IPVSMVEQS NTLNRCKKKS RMTCSSSRSR SCPCATPMRA

1028

```

51  SGRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTLPSLNGLTKVLT
101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKFCF CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

              10      20      30      40      50      60
m645.pep      MMMVLALGISIPVSMVSEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGRVSSRSR
a645          MMMVLALGMSIPVSMVSEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGRVSSRSR
              10      20      30      40      50      60

              70      80      90      100     110     120
m645.pep      IFSIVSTSLCRKNTCPPLRSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
a645          MFSMVSTSLCRKNTCPPLRSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
              70      80      90      100     110     120

              130     140     150     160     170     180
m645.pep      ILKVRGIGVAVMVRISTLARRRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
a645          ILKVRGIGVAVMVRMSTLARRRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
              130     140     150     160     170     180

              190     200     210     220     230     240
m645.pep      STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
a645          STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT
              190     200     210     220     230     240

              250     260     270     280
m645.pep      ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
a645          ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCGAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

```

g647.pep
1  MQRLAADGIQ IFFVGVDGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGTVAVADTV FRQIVGVVDD TDAERTAVHS RGTRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCGAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

```

m647.pep
1  MQRLAADGIQ IFFVSVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

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1029

51 GFKGTVGQTE RGTVAADTV FRQIISIVNH ADAERTAHS RGTRGFYRIS
101 LII*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQR	LAADGIQIFFVSV	DGQFALRINGLV	KERARTVFFGK	VCRCFEQVILY	GFKGTVGQTE
g647	MQR	LAADGIQIFFVSV	DGQFALRINGLV	KERARSVFFGK	VCRCFEQVILY	GFKGTVGQTE
	10	20	30	40	50	60

	70	80	90	100
m647.pep	RGTVAADTVFRQIISIVNHADAERTAHSRGTRGFYRISLII	X		
g647	RGTVAADTVFRQIVGVDDTAERTAVHSRGTRGFYRISLII	X		
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq
1 GTGCAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTGTG TAGGTGTGCA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC CGGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep
1 VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS
101 LII*

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQR	LAADGIQIFFVSV	DGQFALRINGLV	KERARTVFFGK	VCRCFEQVILY	GFKGTVGQTE
a647	VQRLVTHSVQVFFV	VGVDGQFALRING	LVKERARTVFFGK	VCRCFEQVILY	GFKGTVGQTE	
	10	20	30	40	50	60

	70	80	90	100
m647.pep	RGTVAADTVFRQIISIVNHADAERTAHSRGTRGFYRISLII	X		
a647	RGAVAVADTVFRQIIRIVDHADTERTAHSRGTRGFYRISLII	X		
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51 CGACGTTTGT AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATA CGCTTGCGTA TGTTCGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAA TTCGCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAACCCCGAA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATT GCACGCCATA
301 ATCAAGCTGG CGGATACGGT TGTCTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAA GATTGACCG CCGCCTGAAA
451 CATCTTAAAG AAGGGAATGC AGCCGGTATG CCGGCTTCA CCGCCCGGA
501 TTTGCTGTC CAGCCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCG
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1030

```

1  MNRNRNARIER AVRIAVIDVL NVDPAGPGTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVDLHAI
101 IKLADTVVFH APVVFQHQQA FGFNMPQGEV GGCRAAAHAT LTRFRDRLK
151 HLKEGNAAGM FGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 OTIVAFNOHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```
m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGTAT
51  CGACGTTTGT AATGTAGATG CGCCGCGTTC CGGCACGCTC CTGCATCAGC
101 GTGGAATAACA GGTGCGGAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCCTTG TCGGCAAAAA
201 ACCGTTCGTA CAATCCGGA ACCTCGTTGG CGGAAAAACG CGTAATGTTG
251 CGGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCAGCCGCTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCGCGGTTG TTTTCAACA
351 CCAGCAGGCT TCGGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCGCGC TTGCGAACAG CGCTTGACCC CCGGCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGGCTTTCG CCGGCCCCGA
501 TTTTCGTGTC CAACCCGCGG ATACGTCGGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTTCA AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGTATCTCA TCAGCAACACA GCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```
m648.pep
1      MNRRDARIER AVRIavidVL NVdAPGSgtL LHQRGKQVGS RNDALADIRV
51     LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV
101    IKLTDTVVFH TAVVFQHQQA FGFDMPQGV E QGCRAAAHAA LRTGFDRRLK
151    HFKEGNAAGM FRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201    OTVAFAOHT A*
```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDPAGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
g648	:					
	10	20	30	40	50	60
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQA	VDLHAVIKLTDTVVFHTAVVFQHQQA				
g648						
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQA	VDLHAVIKLTDTVVFHTAVVFQHQQA				
g648						
	70	80	90	100	110	120
m648.pep	FGFDMPQGVQGGCRAAAHAALRTGFDRRLKHFK	EGNAAGMPRFAAPDFAVQ	TADTSGIDA			
g648						
	130	140	150	160	170	180
m648.pep	FGFDMPQGVQGGCRAAAHAALRTGFDRRLKHFK	EGNAAGMPRFAAPDFAVQ	TADTSGIDA			
g648						
	130	140	150	160	170	180
m648.pep	DARTLGNVFHN	RAGSGIDGIQTIVAFNQHTAX				
g648						
	190	200	210			
m648.pep	DARTLGNVFHN	RAGSGIDGIQTIVAFNQHTAX				
g648						
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

a648.seq

```
1  ATGAACAGGC  GCAACGCGCG  GATCGAACGG  GCTGTGCGTA  TTGCAGTGAT
51  CGACGTTTTG  AATGTAGATG  CGCCCGGTTT  CGGCACGCTC  CTGCATCAGC
101 GTGGAATAACA  GGTCCGCAGC  CGGAATGATG  CGCTTGCGGA  TATCAGGGTC
151 TTGCTCGTAT  TTCGTATAGA  GCGCCTCAAA  TTCGTCTTGG  TCGGCAAAAA
201 ACGCTTCGTA  CAATCCCGGA  ACCTCGTTGG  GCGAAAACAG  CGTAATGTTG
251 CCGCCCTTAA  TCAGGCGGGT  GTACAGCAGG  CGGTTGATTT  GCACGCCGTA
301 ATCAAGCTGA  CGGATACGGT  TGTCTTCCAC  GCCCGGTTG  TTTTTCACAA
351 CCAGCAGGCT  TTCGGCTTCG  ATATGCCACA  AGGGGTAGAA  CAAGGTTGCC
401 GCGCCGCGCG  GCACGCCACC  TTGCGAACAG  GATTTGACTG  CCGCGTGAAG
451 CATTTTAAAG  AAGGGAATGC  AGCCGGTATG  CGGTGCTTCG  CGCCGCCGGA
```

1031

501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
 551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCTG TCGCATTCTGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGDCRLK
 151 HFKEGNAAGM PCFAAPDFAV QSADTS GIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	:					
	10	20	30	40	50	60
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648						
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648						
	70	80	90	100	110	120
m648.pep	FGFDMPQGV E QGCRAAAH AALRTG FDRRLKH FKEGNAAGM PRFAAPDFAVQTADTS GIDA					
a648						
	130	140	150	160	170	180
m648.pep	FGFDMPQGV E QGCRAAAH AALRTG FDRRLKH FKEGNAAGM PRFAAPDFAVQTADTS GIDA					
a648						
	130	140	150	160	170	180
m648.pep	190 200 210					
a648	DARTLGNVFHN RAGSGIDGIQTIVAFNQHTAX					
	190 200 210					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACCTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAA CATATCAGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTCG ATGATTTCGA CCGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFTLTPYA EQKIQCRAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACCTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTCG ATGATTTCGA CCGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECKRYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCAAAY EAFDDFDGGS
 101 FRR*

m649/g649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECKRYLERRAAWYRSQGN					
g649	MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECKRYLERRAAWYRSQGN					
	10	20	30	40	50	60
	70	80	90	100		
m649.pep	VQELRENKKARKAFRSLPYAEQKIQCAAAYEAFDDFDGGSFRRX					
g649	VQELRENKKARKAFRTLPHYAEQKIQCAAAYEAFDDFDGGRFRRX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

a649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
 51 CGGTGCCCGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
 101 AGGCAAACAA GCAGATGCTG CACCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
 251 CCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCA CCGCAGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

a649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECKRYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKIQCAAAY EAFDDFDGSR
 101 FRR*

m649/a649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECKRYLERRAAWYRSQGN					
a649	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECKRYLERRAAWYRSQGN					
	10	20	30	40	50	60
	70	80	90	100		
m649.pep	VQELRENKKARKAFRSLPYAEQKIQCAAAYEAFDDFDGGSFRRX					
a649	VQELRENKKARKAFRSLPYKEQKIQCAAAYEAFDDFDGSRFRRX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

g650.seq
 1 ATGTCCAAAC TCAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
 51 TCCGGGTTTC CTATATGCC AAAACACCTC ATCACACCAA GTCGGTTTAG
 101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
 151 TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
 201 GGGCGAAGTC AATCCGAAC TGGTACGCC CCACGAAAGC AAATTCATCG
 251 CAAGCCGAG CTATTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
 301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCCG
 351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
 401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
 451 GGCTTGAAA AAACaccgGT TTACGacgGC aggcacGacg TTtacgcaGc
 501 taccgatgcc gcactCAACT AtctGcAATA TCTCTatggA CTGTTGCGCG
 551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
 601 CCGGCCGTC ACGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
 651 CCGCGTATG CCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
 701 TCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

1033

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751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTCAAC GTCCCGCGct tcatCCCCAA AAaacaacgc
901 aaactGCTGC TTCCTGTCCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCTGTTT CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCcggcag gcaCGGTGAA CGTCAGCATT gccGaatcc aacCCgccc
1251 cgcaCAGACA gcggaacatta ccgtcgacc tttgcccga gaaaccgtcc
1301 gtacgggaac ccgatcccc tgtccgcaTt accgaacccg ccctTGCAGC
1351 AGCCGCAGCG CaacctCAA cgcAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pep
1 MSKLKTIALT ASGLSVC PGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGFMRGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAAALL FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSGFMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDYRSN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1 ATGTCCAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGGCGAG CTGGGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGCG AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCCG
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGCG
551 ACTGGCCGCT TGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCGG
701 TGCGCAACAT TATTGCCACT CCCCATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCTAAACCC CGCATTTCAAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAATGCTGCT TTCCTGTCCG GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTGCGCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCC TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pep
1 MSKLKTIALT ASGLSVC PGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGFMRGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAAALL FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSGFMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLKTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGFMRGEVNPVLVRRHESKFIAHSYFNVRVNRSPYMYHIANEVKKRNMPAEALLP					
g650	LRQGFMRGEVNPVLVRRHESKFIAHSYFDRVVNRSPYMYHIANEVKKRNMPAEALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHV GASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHV GASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEVNGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
g650	LFGDWPLAFAAYNWGEVNGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFGMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFGMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDTPYRSNMPAGTVNVGIARIRPAAQQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIDIDNTPDTPYRSNMPAGTVNVSIARIQPAQAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDRAVHX					
g650	ADITVAPLPQETVRTGTRSPCPHYRTPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

```

a650.seq
1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCGTCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGAGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGTACCGG CAGGCATTAC
451 GGCCTGGA AAACACCGGT TTACGACGGC AGGCACGACA TTTACGCCGC
501 CACCGATGCC GCACTCACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAACT GGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTTCCCAAG CTGCTCGCCG
701 TGCGCAACAT CATTGCCGCC CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCGTATTT TCAGGCAGTC GAACCGGACC GTCCGTCGGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCGCGT TCATCCCCAA AAGCAAACGC

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1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```

a650.pep
1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGRMGEV NPVLRRHES KFIASHSYFN RVINRSRPMY
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIIYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEVNGV
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTNYSRN
401 MPAGTVNVGI ARIRPAAQQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

m650/a650 99.1% identity in 465 aa overlap

m650.pep      10      20      30      40      50      60
MSKLKTIALTASGLSVCPGF LYAQTSSHQ IGLAIMRLNSSILDLPPTKQYFQSGSLWGE
|||||
a650          10      20      30      40      50      60
MSKLKTIALTASGLSVCPGF LYAQTSSHQ IGLAIMRLNSSILDLPPTKQYFQSGSLWSE

m650.pep      70      80      90      100     110     120
LRQGRMGEVNPVLRRHESKFIASHSYFN RVINRSRPMYHIANEVKKRNMPAEALLP
|||||
a650          70      80      90      100     110     120
LRQGRMGEVNPVLRRHESKFIASHSYFN RVINRSRPMYHIANEVKKRNMPAEALLP

m650.pep      130     140     150     160     170     180
FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
|||||
a650          130     140     150     160     170     180
FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG

m650.pep      190     200     210     220     230     240
LFGDWPLAFAAYNWGEVNGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
|||||
a650          190     200     210     220     230     240
LFGDWPLAFAAYNWGEVNGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA

m650.pep      250     260     270     280     290     300
PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
|||||
a650          250     260     270     280     290     300
PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR

m650.pep      310     320     330     340     350     360
KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
|||||
a650          310     320     330     340     350     360
KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG

m650.pep      370     380     390     400     410     420
NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNYSRNMPAGTVNVGIARIRPAAQQT
|||||
a650          370     380     390     400     410     420
NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNYSRNMPAGTVNVGIARIRPAAQQT

```

1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDRHAVX					
a 650	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDRHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAACAACAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCGCG CTACAAGGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATACTTGGA GGTGTTGGTTA
551 ACGAATTCCC GATTATTTC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCTGAAAGC cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCAaccgt ccggCGAAAC CGAAGACAGT Accattgccg
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTA AAAaccg TTCTTTGAGc
901 cgtTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCgcctACT ACCCGGCGAA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1  MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANN SLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
201 EGWKKLLTEKL GKKVQLVGDD LFTVNPRIKA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AAYYPGKAAF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAACAACAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAGCGG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGTAGAG TTCAATTGGT
651 TGGCGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAa CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCCGCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1  MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANN SLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

```

1037

```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFPIIS IEDGMDENDW
201 EGWKLKTEKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAIDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

              10      20      30      40      50      60
m652.pep      MIELDGTENKGNLGANATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              |||||
g652          MIELDGTENKGNLGANATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              10      20      30      40      50      60

              70      80      90      100     110     120
m652.pep      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCDSKGFPPTVGVDEGGFAPNLN
              |||||
g652          EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCDSKGFPPTVGVDEGGFAPNLN
              70      80      90      100     110     120

              130     140     150     160     170     180
m652.pep      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              |||||
g652          SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              130     140     150     160     170     180

              190     200     210     220     230     240
m652.pep      GLVNEFFPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
              |||||
g652          GLVNEFFPIISIEDGMDENDWEGWKLLTEKLGKVKVQLVGDDLFVTNPKILAEGIEKGVANA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652.pep      LLVKVNQIGTSETLKAIDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              |||||
g652          LLVKVNQIGTSETLKAIDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              250     260     270     280     290     300

              310     320     330
m652.pep      RSDRMAYNQLLRIEELAEAAADYPSKAAFYQLGKX
              |||||
g652          RSDRMAYNQLLRIEELAEAAAYYPGKAAFYQLGKX
              310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGCG GTGCGAATGC
51  GACTTTGGCG GTTCTATGCG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGCGGGCG CAGGCCCGAT GTCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCGG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAAGCG GCGGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTGGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCTGTGTC
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGCGAAAG TCCAACTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
751 TTGAGTGAAA CCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACGGG TTCTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GNLGANATLA VSMVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```

1038

151 ASSEFYKD GK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
 201 EGWKLLETKL GGVQLVGGDD LFTNPKILA EGIKGVANA LLVKVNIQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

m652.pep	10	20	30	40	50	60
	MIELDGTENKGNLGNATLAVSMVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
a652	MIELDGTENKGNLGNATLAVSMVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
m652.pep	70	80	90	100	110	120
	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDSKGFPPTVGDEGGFAPNLN					
a652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDSKGFPPTVGDEGGFAPNLN					
	70	80	90	100	110	120
m652.pep	130	140	150	160	170	180
	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
m652.pep	190	200	210	220	230	240
	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGVQLVGGDDLFTNPKILAEGIEKGVANA					
a652	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGVQLVGGDDLFTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
m652.pep	250	260	270	280	290	300
	LLVKVNIQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
a652	LLVKVNIQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
m652.pep	310	320	330			
	RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX					
a652	RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

1 ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
 51 CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
 101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
 151 CTTCGCGACG GCGACAAATC CCGCTATTCC GGCAAAGGCG TATTGAAGGC
 201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
 251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
 301 GAAACAAAG GCAATTTGGG TCGCAATGCG ACTTTGGCGG TCTCTATGGC
 351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
 401 TGGGGGCGCG AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
 451 AACGGGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
 501 TATGCCCGTC GCGCGAAAAT CTTTCGCGA AGCGTTGCGC TCGGGTGGCG
 551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGTAAAGG CTTCCCGACC
 601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCGC AACCTGAACA GCCACAAAGA
 651 AGCCCTGCAA CTGATGGTGC AAGCGGCCGA AGCCGCCGCG TACAAGGCGG
 701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
 751 GACGGCAAAAT ACCACTTGGA AGCCGAAGGC CGCTCTACA CCAACGCGGA
 801 ATTTGCCGAA TACTTGGAAG GCTTGGTTAA CGAATTCCTG ATTATTTCCA
 851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
 901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GCGGACGACT TGTTCTGTAAC
 951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
 1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
 1051 GTCGATCTGG CAAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
 1101 CGCGGAAACC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
 1151 GTATGCAGAT TAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
 1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
 1251 CCCCAGCAA GCCGCATTCT ACCAAGTGGG CAAATAA

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

g652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNAN TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVLQV GDDLFTVNP K ILAEGIEKGV ANALLVKVNQ IGTLSSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCCG GAAATTTTGG ACTCAGCGCG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCCGCGACG GCGACAAATC CCGTTATTCT GGCAAGGGCG TATTGAAGGC
201 GGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTGCACGC GCCCGTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGCGCGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGCGC AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAAT CTTTCGCGCA AGCGTTGCGC TCGCGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCGCCGAC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAGA
651 AGCCCTGCAA CTGATGGTCG AGCGCAGCGA AGCCGCGCGC TACAAAGCGG
701 GCGAAGACGT ATTATTGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAAAGTGG GCGGTAGAGT TCAATTGTTT GCGCAGGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CCGCGAAACC GAAGACAGCA CCATTGCGGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAACCCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCAGCAAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNAN TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVLQV GDDLFTVNP K ILAEGIEKGV ANALLVKVNQ IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGA					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGA					
	130	140	150	160	170	180
m652-1	KSFREALR					
g652-1	KSFREALR					

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKL	CDKSGFP	TTVGDEGGF	APNLNSHKEAL	QLMVEATEA	AAGYKAGEDVLFA
g652-1	CGAEIFHALKKL	CDKSGFP	TTVGDEGGF	APNLNSHKEAL	QLMVEATEA	AAGYKAGEDVLFA
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYK	DGKYHLEA	EGRSYTNAE	FAEYLEGLV	NEFPIISIED	GMDENDWEGWKLLT
g652-1	LDCASSEFYK	DGKYHLEA	EGRSYTNAE	FAEYLEGLV	NEFPIISIED	GMDENDWEGWKLLT
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRVQLV	GDDLFTV	NPKILAEG	IEKGVANAL	LVKVNQIG	TLSETLKA
g652-1	EKLGGRVQLV	GDDLFTV	NPKILAEG	IEKGVANAL	LVKVNQIG	TLSETLKA
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGET	EDSTIAD	LAVATNC	MQIKTGS	LSRSDRM	AKYNQLLR
g652-1	SVMSHRSGET	EDSTIAD	LAVATNC	MQIKTGS	LSRSDRM	AKYNQLLR
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCCGCGACG GCGACAAATC CCGTTATTTCG GGCAAGGGCG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAAT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGTCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GGCGCAAAAT CTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGTCTCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAACTGG GCGGCAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCAGCAAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNLSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDKSGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVQLV GDDLFTVNP KILAEGIEKV ANALLVKVNQ IGTLSLTKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1  MSAIVDIFAREILDSRGNPTVECDVLLSGVMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1  MSAIVDIFAREILDSRGNPTVECDVLLSGVMGRAAVPSGASTGQKEALELRDGDKSRY
          10      20      30      40      50      60
m652-1  GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1  GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
          70      80      90     100     110     120
m652-1  AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSNIQEFMIMPVGAKSFREALR
a652-1  AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSNIQEFMIMPVGAKSFREALR
          130     140     150     160     170     180
m652-1  CGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1  CGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
          190     200     210     220     230     240
m652-1  LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
a652-1  LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
          250     260     270     280     290     300
m652-1  EKLGGRVQLVGDDLFVTNPKILAEGLIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1  EKLGGRVQLVGDDLFVTNPKILAEGLIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
          310     320     330     340     350     360
m652-1  SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYKNOLLRIEEELAEAAADYPSK
a652-1  SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYKNOLLRIEEELAEAAADYPSK
          370     380     390     400     410     420
m652-1  AAFYQLGKX
a652-1  AAFYQLGKX
          429

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGct ttgccccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTTCA TCGGTTGCAG GtcgacgaGG
151 AAAacgTGGC TTTCGGTGCG GCCGGAaacy atgcyCaaac cgCGTttaac
201 caactcttcc gccATGACGG CAGCATTGAT TTCACTTGT TTGCGTATT
251 GTTTGAactC GGGTTGcaac gttctTTAA acgctACGGC TttgCGGCG
301 ATAACGTgca tcaACGGAacc gCCTTGcAGG CTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTcACGGCA CAAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTGTGG GTGGTAGTgG ttACgaaGtc GCAGaatggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRME VTYGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAAALFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLV VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTGACGGT GATGTGCGCT TTGCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCACGAGG

```


1042

```

151 AAAACGTGGC TTTCCGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAAGTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTGGG GATATTCGCC GCCGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLITVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

```

m653.pep      10      20      30      40      50      60
MAAEPMRMPEVT KGFSGSFGMA FLITVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||
g653          10      20      30      40      50      60
MAAEPMRMPEVT YGFSGSFGMA FLITVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||

m653.pep      70      80      90     100     110     120
MRKPRLTNSSAMA AALIFTCFAYCLNSGCN ASLNATALAAITCISGPPCRLGKMEEFNAF
|||||
g653          70      80      90     100     110     120
MRKPRLTNSSAMT AALIFTCFAYCLNSGCN ASLNATALAAITCINGPPCRLGKMEEFSAF
|||||

m653.pep      130     140     150     160
SWVLSRHKITPPR GPRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||
g653          130     140     150     160
SWVLSRHKITPPR GPRLVWVVVTKSQNGTGLGYSPPATSPAX
|||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGCGCGCGG AACCGATGCG GATGCCGAG GTAACGAAGS GTTTTCCGG
51  ATCATTCCGG ATGGCGTTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTCA TCGTTGCGAG GTCAACGAGG
151 AAAACGTGGC TTTCCGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAAGTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLITVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

```

m653.pep      10      20      30      40      50      60
MAAEPMRMPEVT KGFSGSFGMA FLITVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||
a653          10      20      30      40      50      60
MAAEPMRMPEVT KGFSGSFGMA FLITVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||

m653.pep      70      80      90     100     110     120
MRKPRLTNSSAMA AALIFTCFAYCLNSGCN ASLNATALAAITCISGPPCRLGKMEEFNAF
|||||
a653          70      80      90     100     110     120
MRKPRLTNSSAMA AALIFTCFAYCLNSGCN ASLNATALAAITCISGPPCRLGKMEEFNAF
|||||

m653.pep      130     140     150     160
SWVLSRHKITPPR GPRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||
a653          130     140     150     160
SWVLSRHKITPPR GPRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||

```

g656.seq

```
1 ATGCCGCGTT TCTCCGGTTC GATTTCCTCG ATGATTTC CA TCGCCGGGAC
51 TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGC ctTCGACGTT GCGAAACGATG
151 TGCATCACAT GGGAGTATTT TTTCAATCACC ATTTTGTCCG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGGcatt TCTTTGGCGT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCCGCGGG CGTTTTCGCG CGCAGCGCGG TGCCGGCGGAT
351 GGGGCGGACG ATGACGTcat GCGTTTCGCC GCGGACGAGG ATTTCCGGCGG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

g656.pep
1 MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPMGRT MTSSRSRRT R ISGEPTMWK SPKS*

```
m656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGCGCAGG GAAGGCTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGCTC TTCACAGCGC CTTTCGACGTG GGAACACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACTTTGAC
201 TTCGCCGGTT TTA CTGATGC GGCCGACGTC GTTGCGTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCCGGCGGT GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TGCGTTCGCG TCGGACGAGG ATTTCCGGCGG
401 AGGAGCCGAC GATGTGGA AA TCGCCGAAAT CGTAG
```

m656.pep
1 MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPS FRRPSTLETM
51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP K SINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPA MGRT ITSLSRRT R ISGEPTMWK SPKS*

Homology with a predicted ORF from *N. gonorrhoeae*

```

                                10          20          30          40          50          60
m656.pep    MPRLLGSTSSMISMARTILGAPESVPAGKVAARMSMLVMPFSRRPSTLETMCITWEYFSIT
              |||: || |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g656         MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTFSPFKQPSTLETMCITWEYFSIT
              10          20          30          40          50          60

                                70          80          90          100         110         120
m656.pep    ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLPRRRVPAMGRT
              |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g656         ILSVTLTSPVLLMRPTSLRPKSI SITCSAISLASLNKSCSLARSSAGVLPRRRVPAMGRT
              70          80          90          100         110         120

                                130         140
m656.pep    ITSLRSRRTRISGEEPTMWKSPKSX
              :|| |||||:||||:||||:||||:||||:||||:||||:
g656         MTSSRSRRTRISGEEPTMWKSPKSX
              130         140

```

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTG GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCCG TAACTTTGAC
201 TTGCGCCGGT TTAATGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTCCGCGGG GGTTTTGGCG CGCAGGCGCG TGCCGGCGAT
351 GGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTCGGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLRSRTRISGEEPTMWKSPKSX					
a656	MTSSRSRTRISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGGCGGTta cgACCGAATT TGAaaacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTCAAGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCGGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattec ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GGCGCAACgc tTGGCGGACG AATTGGATTA TGTCGGCgta
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCCGAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAAcctGCCG
901 cccGccgACA CCAAATTATT aTCCCttgC TGTATGGCGA ATATTTGGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAC CGCACAGAAA
1051 GGTGCGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgc
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pap

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKE	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDELKAAF	AHGGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQARQTAQR	LADEL DYVG

m657.seq

1	ATGAAAAACA	TATCTCTTTC	TCCGCCCGCC	ATGCTTGCCA	TCCTCGCGCG
51	CGGACAATTA	GGCAGAAATGT	TTACCGTTGC	CGCCAAAACC	ATGGGCTACA
101	AAGTAACCGT	TCTCGACCCC	GATCCGGACG	CGCCGGCAGC	AGAATTGCAAT
151	GACCGCCATT	TGTGCGCGCC	GTTTAAACGAC	CAAGCTGCTT	TGGACAGGATT
201	GGCAAAATGC	CGCGCGGTGA	CCACTGAATT	TGAAAACGTC	AATGCCGATG
251	CGATGCGCTT	TTTGGCAAAA	CATACCAATG	TTTCCCCTAG	CGGCGATTGT
301	GTGGCGATTG	CACAAAAACG	CATTCAAGGA	AAGGCATGGA	TACGCCAAGC
351	GGGATTGCAA	ACCGCGCGCT	ATCAAGTGGT	TTGTAAGCTT	GAAGACATCA
401	CTGAAGCAAG	CGCGCAATTT	TTGCGCGCGA	TCTGAAAAC	TGCTACGTTG
451	GGCTACGACG	GCAAAGGTCA	AATCCGCGTA	AAAAATTGG	ATGAACTCAA
501	AGCCGCGTTT	GCGAACACG	GCGGCGTGGA	TTGCGTTTTG	GAAAAAATGG
551	TGATTTCGCG	CAGTGAATTT	TCCGTAAATG	TATGCCGTTT	GAACAATGAC
601	AACGTGCAAA	CTTCGACCC	TGCCGAAAC	ATCCACGAA	ACGGCATCTT
651	GGCTATTTC	ATTCGCCCCG	CGCGACTGAG	TGCCACGTG	CAGCAACAGG
701	CGCGGCAGAT	GCGCAACGC	TTGGCGGACG	AATTGGATTA	TGTCGGCGTA
751	TTGGCGGTAG	AAATGTTTGT	TGTCGGTGAC	ACGCATGAAT	TGGTCGTCAA
801	CGAAATCGCC	CCGCGCCCCG	ACAATTCCGG	ACACCATAAG	ATAGATGCTT
851	GCGCAGCAGA	CGAGTTCCAG	CAGCAGGTAC	GCATTATGTG	CACCTGCGCG
901	CCTGCCGATA	CCAAATTACT	GAGTCTTTCG	TGTATGGCAA	ATATTTTGGG
951	CGACGTTTGG	CAGGAAGACG	GCGGCGAACC	GGATTGGCTG	CCCTTGCAAA
1001	GCCATCCGAA	TGCACACCTG	CACCTTACAG	GCAAAAAAAC	CGCGCACAAA
1051	GGGCGGAAAA	TGGGCAACTT	TACCGTTTTA	ACCACCGATT	CGGACACCGC
1101	ATTTCAAGAA	GCAAAAAAAC	TGCATCAGTC	CCTATAA	

m657.ppt

1	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPDAPAAEFA
51	DRHLCAPIFD	QAALEDELAKC	AAVTTEFENV	NADAMRFLAQ	HTNVSPSGDC
101	VIAQAQNRQE	KAWIRKAGLG	TAPYQGVVCKA	EDITEASAQF	LPGLIKTATL
151	QYDGGKQIRV	KTLDLKAFAF	AEHGGVDCVL	EKMVDLRSEI	SVIVCRNLND
201	NVQTFDPAEN	THENGILAYS	IVPARLSADV	QQQARQMAQR	LADELVDYGV
251	LAVEMFVVDG	THELVNVEIA	PRPHNSGHHT	IDACAADQFQ	QQVRIMCNLP
301	PADTKLLSSC	CAMNIIJGDW	QEDGGEPDWL	PLQSHPNNAH	FLYGKKTAAH
351	GRKMGHFTVL	TTDSDTAFOE	AKDLHOSL*		

Homology with a predicted ORF from *N. gonorrhoeae*

m657/q657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPDPAAPAEFADRHLCAPFND					
	:: : :					
g657	MNTPPILPFPAMLGILGGGQLGRMFVAFAAKTMGYKVTVLDPDPNAPAEFADRHLCAPFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m657.pep	QAALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ					
	: :					
g657	RAALDELAKCAAVTTEFENVNADAMRSLAKHTNVSPSGDCVSIAQNRIQEKAWIRKAGLQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m657.pep	TAPYQVVCKAEDITEASAQFLPGILKTATLGYDGKGQIRVKTLDELKAFAEHGGVD CVL					
	:					
g657	TAPYQAVCKAEDITEASAQFLPGILKTATLGYDGKGQIRVKTLDELKAFAEHGGVD CVL					
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNNDENVQTFDPAENIHENGILAYSIVPARLSADVQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTSDTA FQEAKKLHQS LX					
g657	TTSDTA FQEAKKLHQS LX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGCGCG
51  CGGACAATTA GGCAGAATGT TTA CTGTGTC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTCAGGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GCGCGAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CCGCGTCCGC ACAATCCCGG CCACCATACC GTCGACGCCT
851 GCGCGGCAGA CCAATCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAATTGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGGCCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQARQMAQR LADELNYVGV
251 LAVEMFVVGDTHELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWF PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STSDTA FQE AKKLHQS L*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDA PAAEFADRHL CAPFDN					

a657	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDN	10	20	30	40	50	60
m657.pep	QAALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ	70	80	90	100	110	120
a657	QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ	70	80	90	100	110	120
m657.pep	TAPYQVVKCAEDITEASAQFLPGILKTATLGYDGKGQIRVKTLDDELKAAFAEHGGVDCVL	130	140	150	160	170	180
a657	TAPYQAICKAEDITEESIQFLPGILKTATLGYDGKGQIRVKTVDDELKAAFAEHRGVDCVL	130	140	150	160	170	180
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR	190	200	210	220	230	240
a657	EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQQARQMAQR	190	200	210	220	230	240
m657.pep	LADELNYVGVVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP	250	260	270	280	290	300
a657	LADELNYVGVVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP	250	260	270	280	290	300
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNAHLHLYGKKTAAHKGRKMGHFTVL	310	320	330	340	350	360
a657	PADTKLLSSCCMANILGDVWQEDGGEPDWFLQSRPDAHLHLYGKKTAAHKGRKMGHFTIL	310	320	330	340	350	360
m657.pep	TTSDSDTAFQEAKKLHQSXLX	370	379				
a657	STDSDTAFQEAKKLHQSXLX	370					

g658.seq

```
1 ATGGTGGCCG GAATGTGCG TGC GCGGGGCG GGTTCATTG ACGAGCAATT
51 CATGTGTGTC GCGGACAACA AACATTTCTA CCGCCAAatc GCCGACATAA
101 TCCAATTTCG CCGCCAagcG TTGCGCGCTG TCGCGCGCCT GTGTCTGCAC
151 GTCGGCACTC AGCCGCGcgy gGACGATGga atAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGCGGGGG TCGAAGSTTT GCAGTTTTTC ATCGTTCAGA
251 CGGCATACGA TCACGGAAAT CTCGCGCGCG AAGTCCACCA TTTTTTCCAA
301 AACGCAATCC ACGCGCCGCT GTTCGGCAAA CGGGCTTTG AGTTCGTCCA
351 ACGTTTTGAC CGGGATTTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTAA TGTCTTCGGC
451 CTTGCAAAAC GCCTGATACG GCGCGGTTTG CAAGCCTGCT TTGCGTATCC
501 AGGCTTTTTT CTGAATGCGG TTTTGTGCAA TGGACACGCA GTCGCCGCTG
551 GGGGAAACGT TGGTATGCTT TGCCAGAGAG CGCATCGCGT CGGCAttgac
601 gtTTTCAAAT TCGGTcgtaA CCGCCGCGCA TTTTGCCAAT TCGTCCAACG
651 CGGCCCGGTC GTCAAAACGG GCGCAAAAT GCGGTCGGC AAATTCGCCC
701 CCGCGCGCAT TCGGTCGGG ATCGAGAAC GTTACTTTGT AGCCCATGGT
751 TTTAGCGGCA ACGGCAAAACA TTctgcctAA
```

g658.pep
1 MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRLPRLLLH
51 VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAOVHHEFO

1049

```

101 NAIHAAVFGK RGFEFVQRF ADLTFVAVQA RSRFQDAGQK LRACFSNVFG
151 LANRLIRRGL QACFAYPRFF LNAVLCNGHA VAAGGNVGM LQRAHRVIGID
201 VFKFGRNRRR FCQFVQRGPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
1 ATGGTGTCCG GAATTGTGCG GCGCGGGGCG GATTCGTTG ACGACCAATT
51 CATGCGTGTC ACCGACAACA AACATTTCTA CCGCCAATAC GCCGACATAA
101 TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CCGCATACGA TTACGGAAAT TTCCTGCGC AAATCCACCA TTTTTCCTCA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTTAC GCGGATTGTA CCTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CCGGCAAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTT CAATCCCGCT TTGCGTATCC
501 ATGCTTTTTC CTGAATGCGG TTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGGC GCGCACAAAT GGCGGTCGCG AAATCTGTCT
701 GCCGCGCGT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGTT
751 TTTGGCGGCA ACGGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
1 MVSGIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LRHLPRLLH
51 VGTQSRGDDG ISQDAVEVDV FGRVESLHV IVQTAYDYG NFTAQIHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVAVQA RSRFQDAGQK LRACFSDVFS
151 LTNHLIRRGL QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKFSGHRRR FCQFVQSSLV VKRRAQMAVG KFCRRVRIG VENG YFVAHG
251 FGGNGKHSAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

```

m658.pep      10      20      30      40      50      60
MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLHVGTSRGDDG
||:||||| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
g658          10      20      30      40      50      60
MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLHVGTPRGDDG

m658.pep      70      80      90      100     110     120
ISQDAVEVDVFGRVESLHVIVQTAYDYG NFTAQIHFFQNAIHAAVFGKRGFEFIQCFY
||||| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
g658          70      80      90      100     110     120
ISQDAVEVDVFGGVEGLHVFIVQTAYDHGNLAAQVHHFFQNAIHAAVFGKRGFEFVQRF

m658.pep     130     140     150     160     170     180
ADLTFVAVQRSRFQDAGQKLRACFSDVFSLTNHLIRRGLQSRFAYPCLFLNAVLCNRHT
||||| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
g658         130     140     150     160     170     180
ADLTFVAVQRSRFQDAGQKLRACFSNVFGLANRLIRRGLQACFAYPRFFLNAVLCNGHA

m658.pep     190     200     210     220     230     240
IAARGNIGMFCQKAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRAQMAVGKFCRRVRIG
:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
g658         190     200     210     220     230     240
VAAGGNVGM LQRAHRVIGIDVFKFGRNRRAFQCFVQRGPPVVKRRAQMAVGKFRRRRIRVG

m658.pep     250     260
VENGYFVAHGFGGNGKHSAX

```


1050

```

          :|||||:|||||
g658      IENGYFVAHGFGNGKHSAX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

```

a658.seq
1   ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
51  CATGCGTGTC GCCGACAACA AACATTCTA  CCGCCAATAC GCCGACGTAG
101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
151 GTCGCGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTGTGC ATTGTTCAGA
251 CGGCATACGA TAACGGAAAT TTCGCCGCGC AAGTCCACCA TTTTTCCTCA
301 AACGCAATCC ACGCCGCGGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 CCGTTTGTAC GCGGATTTGG CCTTTGCCGT CATAGCCCAA TGTCGCGGTT
401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
451 TTTGCAAATT GCTTGATACG GCGCGGTTTG CAGGCCTGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGCAGCA TGGCAACGCA GTCGCGCTG
551 GGGGAAACAT TGGTATGTTT GCGGAGAAAA CGCATCGCAT CGGCATTGAC
601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG
651 CGGTTTGTTT GTCAAACGGC GCACACAAAT GGCGGTCGGC AAATTCGCT
701 GCCGCGCAT TCGGTTGGG ATCAGTACG GTTACTTTGT AGCCCATGGT
751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

```

a658.pep
1   MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGOT LRHLSRLLLN
51  VGTQSGWDDG VGEDTVFVNV FGRIESLHV IVQYAYDNGN FAAQVHHFFQ
101 NAIHAAVFGK RGFEFIHRFD ADLAFVIAQ CSGFQDAGQK LYAFFSDVFG
151 FANCLIRRLG QACFAYPCLF LNAVLRDNGA VAAGNIGMF GEKTHRIGID
201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFRCRIRRVG IEYGYFVAHG
251 FGSNSKHSAX*

```

m658/a658 75.3% identity in 259 aa overlap

```

          10      20      30      40      50      60
m658.pep  MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLHVGTSRGDDG
          ||:||||:| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a658      MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGOTLRHLSRLLNVGTQSGWDDG
          10      20      30      40      50      60

          70      80      90      100     110     120
m658.pep  ISQDAVFVDVFGRVESLHVIVQYAYDNGNFTAQIHFFQNAIHAAVFGKRGFEFIQCFY
          ::||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a658      VGEDTVFVNVFGRIESLHVIVQYAYDNGNFAAQVHHFFQNAIHAAVFGKRGFEFIHRFD
          70      80      90      100     110     120

          130     140     150     160     170     180
m658.pep  ADLTFVAVQSRFQDAGQKLRFCSDFSLTNHLIRRLQSRFAYPCLFLNAVLCNRHT
          ||:||||:| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a658      ADLAFVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLQACFAYPCLFLNAVLRDNGA
          130     140     150     160     170     180

          190     200     210     220     230     240
m658.pep  IAARGNIGMFCQKAHRIGIDVFKFSGHRRFCQFVQSSLVVKRRAQMAVGKFCRRVRIG
          :|| ||||| :||:|||||:||||:|||||:|||||:|||||:|||||:|||||:|
a658      VAAGNIGMFGEKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFCRRIRRVG
          190     200     210     220     230     240

          250     260
m658.pep  VENGYFVAHGFGNGKHSAX
          :| |||||:|||||
a658      IEYGYFVAHGFGSNGKHSAX
          250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

```

g661.seq
1  ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151 ACCGGAAAAA CCctgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
201 TGCCGTGCAG ATTGCCGGCA GCGACCccga acaGATGGCG Gatgcgccgc
251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351 CGAGccgctg gttgcCgcca tTTtgaggc ggtggtcAAG GCGGCGGgcy
401 TACCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
451 ctgcCcgccg tcgccaaaat cgccgaagat tgcggcatg ccgccCttgc
501 cggtccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GGcgcGTTAC
551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601 CGGCGACATC actTCgcgcg AAAAAGCCGC CGccgTCCTC AAACAAACCG
651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
701 TTCCGCGATT TGAAGCATTa TGCCGAACAC GCGGTTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
801 ACGCGTTTTa TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGGCGAAAT GCCCGACGGC GAACAGGCGC GGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
1  MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
51  TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDQON
151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
251 EFGRMQSRHF EPHPRHARVL WXDRCARHRT QTHRLVHRRN ARRTTGA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGACCCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAAAG CGTCGTCGCT GCGGCAGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 TTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TCGGGCATCG CCGCCCTTGC
501 CGTCC.AC GG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTCT AAACAAACCG
651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
701 TTCCGCGATT TGAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCACATC CGCGCCATAC
801 ACGCGTTTTa CCGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPRFETL CRTRCFAACL
251 EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTTDS*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCDGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDDQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRNRRRHYDRARRARQAVVLPFRFETL					
g661	GALRTHRRDQKPSHPGLGQRRHHFAAKSRRRPQTNRNRRRHDRARRARQAVVFPFRFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFACLEFGRMQSRHFEPHPRHARVLWXDRRCAHRTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAAA GCGGCGGGCG
401 TACCCGTTAC CCTCAAACC CGTTTGGGTT GGCACGACGA CCATCAAAC
451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCAGCGCG ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCG TCTGGGTCAA
601 CGGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTTA CGGCGACACC GCCGTGTGTC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQQMA DAARYNVSLG AQLIDINMG
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRYLAAKSP SRPQTNRNRR HYDRARRARQ TVVLPFRFETL RRTRCFACLE
251 EFGRMYRHYF EPHPSHARVL RRRRRCARHT QTHRLVHRRN ARRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCDGAGWAVCEMLTSDPTLRNTRKTLHRSDF					

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10          20          30          40          50          60

           70          80          90          100         110         120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70          80          90          100         110         120

           130         140         150         160         170         180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130         140         150         160         170         180

           190         200         210         220         230         240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNNRRRRHYDRARRARQAVVLPREFTL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNNRRRRHYDRARRARQTVVLPREFTL
           190         200         210         220         230         240

           250         260         270         280         290         299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           250         260         270         280         290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGTctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCGGAC GCAACAATTC GGTTTTGTG
601 GATTTTTCG GCATtcagaC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTGGAAATC CTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTGA TCGAAGAACG
801 CGTGCCGCAA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLQFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VELIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRRNSVFP
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTIQ FYPAWKSEFS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTGAAACA

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1054

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CCGCGCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTG
601 GATTTTTTCG GTATTTCAGAC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTTA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTGG GCTGCACAAG CGTTTAAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51  KCFSEWSEEK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNRDSVFE
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PVREADNTVT LH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP RRRIGEINLAKCFSEWSEEK					
g663	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP RRRIGEINLAKCFPEWDEEK					
	10	20	30	40	50	60
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVILYPHFT					
g663	RKTVLKQHFHMAKLMLEYGLYWYASAKCLKSLVRYRNKH YLDDALAAGEKVILYPHFT					
	70	80	90	100	110	120
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
g663	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
	130	140	150	160	170	180
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LH					
g663	SAPFLYLPDQDFGRNNSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LQ					
	190	200	210	220	230	240
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
g663	FYPAWSFPGSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAATT
51  TCTGCCGTTT GCGCTGCTGC ACAAACTGCT TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTTGGCA

```

1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TCGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTT
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTG
601 GATTTCCTCG GTATTTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGGAATC CTTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTGA TCGAGGAACG
801 CGTGGCGGAA CATCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

```

a663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51  KCFPEWDGKK RKTVLKQHEK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVVF
201 DFFGIRTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWESFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

m663/a663 96.2% identity in 293 aa overlap

10 20 30 40 50 60
m663.pep MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK
a663 MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFPEWDGKK
10 20 30 40 50 60

70 80 90 100 110 120
m663.pep RKTVLKQHEKFMMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT
a663 RKTVLKQHEKFMMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT
70 80 90 100 110 120

130 140 150 160 170 180
m663.pep AFEMAVYALNQDIPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
a663 AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
130 140 150 160 170 180

190 200 210 220 230 240
m663.pep SAPFLYLPDQDFGRNDSVVFDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVTLH
a663 SAPFLYLPDQDFGRNDSVVFDFFGIRTATITGLSRIAALANAKVIPAIPVREADNTVTLH
190 200 210 220 230 240

250 260 270 280 290
m663.pep FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX
a663 FYPAWESFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
250 260 270 280 290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

```

g664.seq
1  ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGAcgg gCGGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTGGGGGAA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGAAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAT TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCCT TGTTCCTCAT CGCGCCCAT
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCggaagcgc gtttcgtcCc acttcacgcC gtTTTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTC

```

551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

```

g664.pep
1  MIHPHHFRAF  FINGHGVEIV  HLLIADGAHR  MGRACVFGE  LVLAQQADV
51  DAAHGAAGAV  AGKLLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEIFVSDHG
101 FNAFEIGIGG  GAAVGEDELG  VKNVQTLVFH  RAHIEIAYGD  DHENIQVIFQ
151 PEARFVPLHR  VFSTIPRQSR  PWVCPLRWCK  TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

```

m664.seq
1  GTGATACATC  CGCACTACTT  CCGCGCCTTT  TTCATAAAGC  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TAGCTGGCGG  GCGGCACCGG  ATGGGCGGTC
101 GGGCCTGCGT  CTTGCGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTC
151 GATGCGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTCGC
201 GGAACACGGT  CAGCCCTTCC  TTCAGCGAAA  GCTGGAACCA  GTCGCGGCAG
251 GTTACGCGGT  TGCCCGTCCA  GTTGTGGAAA  TACTCGTGTC  CGACCACGGA
301 TTCGATGCCT  TCGAAATCGG  TATCGGTGGC  GGTGCGGCTG  TCGGCAAGGA
351 CGAACTTGGT  GTTAAAGATG  TTCAAACCTT  TGTTTTCCAT  CGCGCCCAT
401 TTGAAATCGC  CCACGGCGAC  GACCATGAAA  ATATCCAAGT  CGTATTCCAA
451 ACCGAAGCGC  GTTTCGTCCC  ATTTTCATCG  GTTTT.CAA  CGATTCCACG
501 GCAAAGCCGA  CCTTGGGCTT  GTCCGCTTCG  GTGGTGTAAG  ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

```

m664.pep
1  VIHPHYFRAF  FINGHGVEIV  HLLIAGGAHR  MGRACVFGE  LVLAQQADV
51  DAAHGAAGAV  AGKFLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEILVSDHG
101 FDAFEIGIGG  GAAVGKDELG  VKDVQTLVFH  RAHIEIAHGD  DHENIQVVFQ
151 TEARFVPFHR  VFXTIPRQSR  PWACPLRWCK  TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFF	FINGHGVEIV	HLLIAGGAHR	MGRACVFGE	LVLAQQADV	FDAHGAAGAV
g664	MIHPHHFRAFF	FINGHGVEIV	HLLIADGAHR	MGRACVFGE	LVLAQQADV	DAAHGAAGAV
	10	20	30	40	50	60
m664.pep	AGKFLVAEHG	QPFLQRKLEP	VAAGYAVARP	VVEILVSDHG	FDAFEIGIGG	AAVGKDELG
g664	AGKLLVAEHG	QPFLQRKLEP	VAAGYAVARP	VVEIFVSDHG	FNAFEIGIGG	AAVGEDELG
	70	80	90	100	110	120
m664.pep	VKDVTQTLVF	RAHIEIAHGD	DHENIQVVFQ	TEARFVPFHR	VFXTIPRQSR	PWACPLRWCK
g664	VKNVQTLVF	RAHIEIAYGD	DHENIQVIFQ	PEARFVPLHR	VFSTIPRQSR	PWVCPLRWCK
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

```

a664.seq
1  GTGATACATC  CGCACCCTT  CCGCGCCTTT  TTCATAAAGC  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TATCGGCGG  GCGGCACCGG  ATGTGCGGTC
101 GGACCTGCGT  CTTGCGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTC
151 GATACGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTCGC

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1057

```

201 GGAACACGGT CAACCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCTT TGTTTCCAT CGCACCCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPPHFRAF FINGHGVEIV HLLISGGAHR MCGRTC VFGE LVLAQQADV
51  DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

              10      20      30      40      50      60
m664.pep    VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRAVFGELVLAQQADVFDAAHGAAGAV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664         VIHPPHFRAFFINGHGVEIVHLLISGGAHRMCGRTC VFGE LVLAQQADVFDTAHGAAGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m664..pep   AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVKGDELG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664         AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
              70      80      90      100     110     120

              130     140     150     160     170     180
m664.pep    VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVFXTPRQSRPWACPLRWCK
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664         VKDVQTLVFHRTHEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
              130     140     150     160     170     180

m664.pep    TRFX
              |||
a664         TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGg acgaaacgcg cttcgGgttg GAAtatgact tggatatttt
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCACTTC CCCGAAGACG CAGGCCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGCGAAG TGGTGCGGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTcCaacg CCACGACGGA CAGGCAGTGA
551 CTGCGACGTA TTCCGCGCGG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCACTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGGAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTTGA GTTAACCATT AAACAAACCG
701 TGCCGCCCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAACGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCCAG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

```



```

1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTGCGCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAA ctGTGGGACG GCACGAAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcgcg aagCaggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCCG
1351 AACGTCTGCC GCGCCTtcgt cctGCGCGCC GACCCCGCGC acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAcAA gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTGCGC CTTATCGGCT CAAGccgccc cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTGCG TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTCCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

```

g665.pep
1 MKWDETRFGL EYDLDFIMV AVGDfNMGM ENKGLNIFNT KfVLADSRtA
51 TDTDFEGIES VVGHEYfHNW TGNRVtCRDW fQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPtAHP VRpVSyEEMN NFyTMTvYEk
151 GAEVVRMYHT LLGEEGfQKG MKLYfQRHDG QAVtCDDfRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVpPTpDM ADKQpMMIPV
251 KVGLLNRNGE AVAFDYQGKR ATEAVLLMTE AEQAFpLEGV TEAVVpSLLR
301 GFSAPVYLNY PYSDDDL LLL LAHDSDAfTC WEAAQTLyRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDL LDNAfKA LLLGVpSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRfLP KWHELDfRQAA KQENQSYEYS PETADWRtLR
451 NVCRAfVLRA DPAHIETVAE KYGEMAQNMt HEWGILSAVN GNEsDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTLQh PKfSLENPNK
551 ARSLIGSFsR NVPHfHAQDG SGyRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

```

m665.seq
1 ATGAAATGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTCGAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAgTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCG
401 CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CTTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAGTTCG CCTTGtGGTA CAGCCAGGCG GGCACGCCCC TTTTGGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCCCA GCCCGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACtAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CAGCCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTTGTGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTTCA
1251 CTTCTGCGG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CAGCTGCGC

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1059

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCGC CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTCGAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGAGGTC GCCGCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
1  MKWDETRFGL EYDLDFIMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
51  TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNIFELTV KQTVPTPDM TDKQPMIPV
251 KVGLLLNRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAQOTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAA KQENQSYEYS PEAAGWRTLK
451 NVCRAFLVRA DPAHIETVAE KYGEMAQNT HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES					
g665	MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES					
	10	20	30	40	50	60
	70	80	90	100	110	120
m665.pep	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQHOF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
g665	PEDAGPTAHPVRPVSYEEMNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPTPDM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m665.pep	TDKQPMIPVKVGLLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEVTEAVVPSLLR					
g665	ADKQPMIPVKVGLLLNRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEEAAQTLYRRAVAANLATLSDGVLPKHEK					
g665	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEAAQTLYRRAVAANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
g665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAGWRTLNRVCRAFLRADPAHIETVAEKYGEMAQNMT					
g665	KWHELDROAAKQENQSYEYSPETADWRTLNRVCRAFLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
g665	PKFSLENPNKARSLIGSFSRNVPHFHAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
g665	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

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a665.seq
1  ATGAAGTGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
51  CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGTGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGTACCGCC
151 ACCGATACCG ATTTTGAAGG CATCGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACTGG ACGGGCAACC GCGTGACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGTTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGTATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGTCCGAC CGCACATCCG GTGCGCCCGC
401 CCCGATATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGCGAAG TGGTGCGGAT GTATCACACC TTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGT ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCTGTTA
551 CCTGCGACGA TTCCGCGCG GCGATGGTGG ACGCGAACGG CATCAACCTC
601 GACCAATTTC CCTTGTGGTA CAGCCAAGCA GGTACGCCGG TTTTAGATGC
651 TCAAGGGCGT CTGAAAAACA ATGTGTTTGA GTTAACCATC AAACAAACCG
701 TGCCGCCAC GCGCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAATCGGGC TGCTGAACTG CAACGGCGAA GCGGTGGCAT TTGATTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CCTTCCAGTT CGAAAGCGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAATAT CCGTACAGCG ACGACGACCT
951 GCTGCTTCTG CTCGCCCATG ACAGCGACGC CTTACGCGCG TGGGAAGCCG
1001 CACAAACGCT CTACCGCCGT GCCGTCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCGTCG AGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTCA GACGACCTCT TAGACAACGC TTTCAAAGCC CTGCTTTTGG
1151 GTGTGCCGTC TGAAGCCGAG CTGTGGGACG GCGCGGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATATAC TTGCCGTCGG
1251 CTTTCTGCCG AAATGGCAGC AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAGTACAGC CCCGAAGCCG CCGGTTGGCG CACGCTGCGC
1351 AATGTCTGCC GCGCCTTCGT CCTGCGCGCC GATCCGCGCG ACATCGAAAC

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTGCGC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTAGCCGC AACGTCCCGC ATTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCGCC TGGTGCAGGC GTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
1  MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA
51  TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDC QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPPTPDM ADKQPMPIPV
251 KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQAAA KOENQSYEYS PEAAGWRTLK
451 NVCRAEVLRA DPAHIETVAE KYAEMAQNMT HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRSRSD LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHAEADG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

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m665/a665 97.3% identity in 638 aa overlap

m665.pep	10	20	30	40	50	60
	MKWDETRFGLEYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATD					
a665	10	20	30	40	50	60
	MKWDETRFGLEYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATD					
m665.pep	70	80	90	100	110	120
	VVGHEYFHNWVTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
a665	70	80	90	100	110	120
	VVGHEYFHNWVTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
m665.pep	130	140	150	160	170	180
	PEDAGPTAHPVRPASYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDC					
a665	130	140	150	160	170	180
	PEDAGPTAHPVRPARYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDC					
m665.pep	190	200	210	220	230	240
	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPTPDM					
a665	190	200	210	220	230	240
	QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTVPPTPDM					
m665.pep	250	260	270	280	290	300
	TDKQPMPIPVKVGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVPSLLR					
a665	250	260	270	280	290	300
	ADKQPMPIPVKIGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLR					
m665.pep	310	320	330	340	350	360
	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLATLSDGVELPKHEK					
a665	310	320	330	340	350	360
	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLAALSDGVELPKHEK					

1062

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
a665	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRIAQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQIRIAQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTTCTGAA ACCGAAGTGC ATTTTCGACAT TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAAAC TTTGTCCGTC AAAATCAACG GCGCGGGCGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACACAAA
301 TCGCTGATGG GGTGTATGCT TTCCGGCGGC AATCTGTTTA CCCAGTGCAG
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG AAAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTG GCGGTAACGG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTTGGAA TATGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTAGGCGATT TCAATATGGG CGCGATGGAA AACAAAGGTT TGAACATTTT
801 TAACACCAAG TTCGTCTCTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCGCG
1001 CCGTGCCCGC CATCGAGAAC ATCCGCCTGC TGCGCCAGAA CCAGTTCCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGTG CGCCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCATACCCTG CTCGCGCAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATT
1251 CCGCGCGGCG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGAAGCCGA AGGCCGCTG
1351 AAAACAATG TTTTCGAGTT AACCATTAAG CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCCGGCTTC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCT ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGTCTGAT GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAAAC GAAGCCGTCT TTCCCTCGCT GCTGCGGGG TTCAGCGGCG
1601 CAGTGTATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCACGACA GCGACGCTTT CACGTGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCCGCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCGTCCGA
1851 AGCCGAACTG TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGCGCGCGCA AGCCTTGTTG GATACGCTT CCGTCCGCTT CCTGCCGAAA
1951 TGGCACGAAT TGGACCGTCA GCGGCGGAAG CAGGAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAGATT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCCGCCCTT
2251 ATCGGCTCAA GCCGCCGAG CGACACCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AATTTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG AATTGCAGTG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDDRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDFMVVA
251 VGFDFNMGAME NKGLNIFNTK FVLADSRAT DTDFTGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQFSGDR AGRVRRRIEN IRLLRQNFPP
351 EDAGPTAHPV RPSYEEEMNN FYTMTVYKAG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPTPDMA DKQPMMPVK VGLLNRRGEA VAFDYQKRA
501 TEAVLMTTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLYNP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNFAFKAL LLGVPSEAEI WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLRLN VCRFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSRRSDTL QVQVQALQHP KFSLENPNKA RSLIGSFSRN VPHEHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTATC ATTTTGATAT TAATGAACCG CAAACCGCTG
101 TGAAGTCGCG TTTGACGGTT GAGCCGCGA GGTAGGGGA GCCGCTGGTG
151 TTTGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGCGGCG
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGCTCG
251 AACGCTTCAC GTCGAAGTG GAAACCGAAA TCCTGCCGCG GGAACAACAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACCACCACC ATCGTCGCGC AAAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTCCG GGGCGATTG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTATC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGA TACGACTTGG ATATTTTCAT GGTGCTCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCCTTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGGCGCG CATCGAAAAC ATCCGCTGCG TGCGCCAGCA CCAGTTCCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCCGCCA GCTATGAGGA
1101 GATGAACAA TTCTACACCA TGACCGTTTA TGAAGGAGGC GCGGAAGTAG
1151 TGCGGATGTA TCACACCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTATCCT GCGACGATTT
1251 CCGCGCGCGG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCCGCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGAAGCGGA AGGTCTGCTG
1351 AAAAAAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCACGCGC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTTC ACTATCAGGG CAAACGCGCG

```

1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CCGTGCACTCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCGCGGCCA ACCTTGCCAC GCTTTCAGAC GGCGTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTTCAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCGGAGCTG TGGGACGGCG CAGAAAAATC CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAAAAC AAAGCTACGA
2001 ATACAGCCCC GAAGCCGCGG GCTGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGTCTT GCGCGCGGAC CCGCGGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCCTC
2251 GTCGGCTCAA GCCCGCGCAG CGACACCTG CAACAGGTTG GAACCGCCTT
2301 CGAGCATCCG AAATTCAGCC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGTCCGC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCAACG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGGGCG
2551 CAGGAAGGAT TGTGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTETYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQP
351 EDAGPTAHVP RPASYEEMNN FYTMTVYERK AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDFFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPTPDMT DKQPMPIPVK VGLLNRNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFLEGLVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVELPKHEKL LAAVEKVIDS
601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNQAAK QENQSYEYSP EAGWRTLRN VCRFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AQAADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVG EIVGKILD*

m665-1/g665-1 96.1% identity in 866 aa overlap

	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
g665-1	MSKTVRYLKD	YQTPAYRIE	TELHFDIAEP	QTVVKSRLTV	EPQRVAGEPLV	LDGSAKLLSV
	70	80	90	100	110	120
m665-1.pep	KINGAAADYV	LEGETLTIAG	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
g665-1	KINGAAADYV	LEGETLTIAD	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
	130	140	150	160	170	180
m665-1.pep	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS
g665-1	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFAKPS
	190	200	210	220	230	240
m665-1.pep	YLFALVAGDL	AVTETYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
g665-1	YLFALVAGDL	AVTETRFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
	250	260	270	280	290	300
m665-1.pep	YDLDFIMVVA	VGDFNMGAMEN	NKGLNIFNTK	FVLADSRAT	DTDFEGIESV	VGHEYFHNWT
g665-1	YDLDFIMVVA	VGDFNMGAMEN	NKGLNIFNTK	FVLADSRAT	DTDFEGIESV	VGHEYFHNWT

	250	260	270	280	290	300
	310	320	330	340	350	360
m665-1.pep	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQHQPEDAGPTAHPV					
	370	380	390	400	410	420
m665-1.pep	RPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
	430	440	450	460	470	480
m665-1.pep	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMDKQPMMPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMDKQPMMPVK					
	490	500	510	520	530	540
m665-1.pep	VGLLNRRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRRNGEAVAFDYQGKRATEAVLLLTEAEQAFPLEGVTEAVVPSLLRGFSAPVYLNYP					
	550	560	570	580	590	600
m665-1.pep	YSDDDLNLLLAHDSDAFTRWEEAQTLYRRVAANLATLSDGVELPKHEKLLAAVEKVISD					
g665-1	YSDDDLNLLLAHDSDAFTCWEAQTLYRRVAANLAALS DGIGL PKHEKLLAAVEKVISD					
	610	620	630	640	650	660
m665-1.pep	DLNDAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNRRQAAK					
g665-1	DLNDAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDRAAK					
	670	680	690	700	710	720
m665-1.pep	QENQSYEYSPAAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHWGLSAVNG					
g665-1	QENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHWGLSAVNG					
	730	740	750	760	770	780
m665-1.pep	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQRTALQHPKFSLENPNKA					
g665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQRTALQHPKFSLENPNKA					
	790	800	810	820	830	840
m665-1.pep	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	850	860				
m665-1.pep	VKQALQIRIAQEGLSKDVGEIVGKILDX					
g665-1	VKQELQCIRIAQEGLSKDVGEIVGKILGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC ATTTTGATAT TAACGAACCG CAAACCATTG
101 TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGCGG AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAA
301 TCGCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTTA CCCAGTGC GA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGGG ACAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GGCGAGTATT CAGACGGCGG

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501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTC GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGA TACGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTGGGCGATT TCAATATGGG TCGATGGAA AACAAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCCTTG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGGCGCG TATCGAAAAC ATCCGCCTGC TCGCCAGCA CAGTTCCCC
1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCCGCCG GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGCG GCGGAAGTGG
1151 TGCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTTACCT GCGACGATT
1251 CCGCGCGGCG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTGCGCT
1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAACAATG TGTTTCGAGT AACCATCAA CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA ATCGGGCTGC
1451 TGAATGCAA CGGCGAAGCG GTGGCATTTC ATTATCAGG CAAACGCGCG
1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GTCGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA GCGACGCTT CACGCGTGG GAAGCCGAC AAACGCTCTA
1701 CCGCCGTGCC GTCGCGGCGA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGCCGAAACA CGAAAACTG CTTGCCGCGC TCGAAAAAGT CATTTAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGCTCTG
1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCGCTG CGTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAAACC AAAGTACGA
2001 GTACAGCCCG GAAGCCGCGG GTTGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGCGA TCCTGTCCCG
2151 CGTCAACGCG AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTC
2251 GTCGGCTCAA GCCGCCGAG CGACACCCG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAAGCC CGCTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGCGAGC
2401 GGTACCCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGGTCGCG GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCAACG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGGGCGG
2551 CAGGAAGGAT TGTGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMLGYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYS DGRHWV KWEDPFAKPS YLFALVAGDL AVTETYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTD FEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRHQHQP
351 EDAGPTAHVP RPARYEEMNN FYTMTVYERK AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPTPDMA DKQPMPIPVK IGLLNCNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHSDAFTRW EAAQTLYRRA VAANLAALSD GVLPKHEKL LAAVEKVIDS
601 DLLDNAFKAL LLGVPSEAE LWDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNROAAK QENQSYEYSP EAAGWRTLRL VCRAFVLRAD PAHIETVAEK
701 YAEMAQNMTH EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QVQVQALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRENQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
851 QEGLSKDVG EIVGKILD*

```

a665-1/m665-1 97.2% identity in 867 aa overlap

```

          10      20      30      40      50      60
a665-1.pep MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV
          |||
m665-1      MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV
          10      20      30      40      50      60

          70      80      90     100     110     120

```

a665-1.pep	KINGVAADYVLEGETLTIADVPSERFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFS DGRHWVKWEDPFSKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGFVAVESLKNAMKWDETRFGLE
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGFVAVESLKNAMKWDETRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
	YDLDFIMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATDTDFEGIESVVGHEYFHNWT
m665-1	YDLDFIMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATDTDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
	RPARYEEMNNFYTMVYKGAEVVRMYHTLLGEEGFQKGMKLYFQRHGDQAVTCDDFRAA
m665-1	RPASYEEMNNFYTMVYKGAEVVRMYHTLLGEEGFQKGMKLYFQRHGDQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
	MVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTVPTPDMDKQPMMPVK
m665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPMDTKQPMMPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
	IGLLNNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
m665-1	VGLLNNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
	YSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVANLAALSDGVLPKHEKLLAAVEKVISD
m665-1	YSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVANLATLSDGVLPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
	DLLDNAFKALLGVPSEAEWDGAENIDPLRYHQAREALLDILAVRFLPKWHELNROAAK
m665-1	DLLDNAFKALLGVPSEAEWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNROAAK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
	QENQSYEYSPEAAGWRTLNRVCRAFLRADPAHIETVAEKYAEQAQNMTHWGISAVNG
m665-1	QENQSYEYSPEAAGWRTLNRVCRAFLRADPAHIETVAEKYGEQAQNMTHWGISAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
m665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
m665-1	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL

1068

```

          790      800      810      820      830      840
          850      860
a665-1.pep VKQALQRIRAQEGLSKDVGEIVGKILDX
            |||||
m665-1     VKQALQRIRAQEGLSKDVGEIVGKILDX
            850      860

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1   ATGCTTTGTA TGAATTATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTAGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTGT GTATTGGGAC AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1   MLCMNYSNS GEGVLVAKTY LLTALIMSMV ISGQVIHAN QGKVNTHSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1   ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTGT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1   MPCMNHQNS GEGVLVAKTY LLTALIMSMT ISGQVIHAN QGKVNTHSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

```

          10      20      30      40      50      60
m666.pep MPCMNHQNSGEGVLVAKTYLLTALIMSMTISGQVIHANQGKVNTHSAVITGADAHTPE
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g666     MLCMNYSNSGEGVLVAKTYLLTALIMSMTISGQVIHANQGKVNTHSAVITGADAHTPE
          10      20      30      40      50      60
          70      80      90     100     110     120
m666.pep HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGSAAADAMVAVQTTLSEVPQSSGL

```

```
a666.seq
  1  ATGCCTTGTA  TGAATCATCA  ATCAAACCTCA  GGCGAAGGAG  TGCTTGTGGC
51  TAAACATAT  TTATTGACTG  CATTGATAAT  GTCTATGACA  ATCTCTGGAT
101  GTCAAAGTCAT  CCATGCCAAT  CAAGGTAAGG  TTAATACTCA  TTCTGCTGTC
151  ATCAGAGGTG  CAGACGCTCA  CACGCTGAA  CATGCAACGG  GACTGACCGA
201  ACAAAGCAG  GTGATTGCAA  GTGATTTTAT  GGTAGCGTCA  GCCAATCCAT
251  TAGCAACACA  AGCTGGCTAT  GATATCTTAA  AGCAAGGCGG  TAGCGCTGCA
301  GATGCGATGG  TGGCGGTGCA  GACGACACTA  AGCTTGGTAG  AGCCACAGTC
351  GTCAGGCTTG  GGCGGTGGTG  CATTTGTGTT  GTATTGGGAT  AATACCGCCA
401  AACATTGAC  CACATTTGAT  GGGCGTGAGA  CGGCACCGAT  GCGTGCAGCG
451  CCGGAATTAT  TTTTGGATAA  AGATGGTCAA  CCATTGAAAT  TTATGGAAGC
501  GGTGGTCGTG  GTCGCTCGGT  GGGTACGCCT  GCTATCCCTA  AACTGA
```

```
a666.pep
  1  MPCMNHQSNS  GEGVLVAKTY  LLTALIMSMT  ISGCQVIHAN  QGKVNTHSAV
51  ITGADAHTPE  HATGLTEQKQ  VIASDFMVAS  ANPLATQAGY  DILKQGSAA
101 DAMVAVQTTL  SLVEPQSSGL  GGGAFVLYWD  NTAKTLTTFD  GRETAPMRAT
151 PELFLDKDGQ  PLKFEAVVVV  VARWVRLLSL  N*
```

m666.pep	10	20	30	40	50	60
	MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
a666	MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
	10	20	30	40	50	60
m666.pep	70	80	90	100	110	120
	HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
a666	HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
	70	80	90	100	110	120
m666.pep	130	140	150	160	170	180
	GGGAFVLYWDNTAKTTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
a666	GGGAFVLYWDNTAKTTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
	130	140	150	160	170	180
m666.pep	NX					
a666	NX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1 atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51 tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAAttgcy
151 GAtttccttc agcgtgcccgc cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTcgcCat atcgtccagC
251 GGCACATTcg ccttcggctG GTAAAGCGCG AGCAAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GCGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCAC TCGTCATCCG GCAGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ActTGCGCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1 MRFVFC LGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51 DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVE IAVARIPIAR GVDVYQGAV MQYGQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMLVLPP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHEFVIRQR RQVIQRTDTL HIGYGFNIES
251 QNRHGSTLH SKTDLRLLLCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1 ATGCGGCTTT TCCCGGCTT GTGCGGACAG GTAATTCGCG ATCCGTTTGA
51 TTTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTGCGCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCAC TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1 MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFIIA
51 DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVE IAVAHIPIAR GVDVYQGAV MQYQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHL
201 MKMMLHKIAA RLSTAEVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

          10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFIIADFLQPARMEC
          ||:  | |::  | ||:||||:| |||||:| | : : ||||| | | | | |
```

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```

g667      MRFVFLGGEIVSDPCDFHLVFRVESAADQTETQIHQIRIHGIGFAIADFLQPARVER
           10      20      30      40      50      60

           70      80      90      100     110     120
m667.pep  LPNLAHVHTQLARKTAQFRHIVQRHVCPRLVKREIQIHQIAVALVITADVVPLEIAAAVE
           ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g667      FPHFAVHTQLARKAAQFRHIVQRHIRPRLVKREIQIHQIAVALVITADVVPLEIAAAVE
           70      80      90      100     110     120

           130     140     150     160     170     180
m667.pep  IAVAHIPIARGVDVAVYQGAVMQYGGQIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g667      IAVARIPIARGVDVAVYQGAVMQYGGQVETAAVPADQLRRMFFNQFEKLGNDHFFAIVHLAD
           130     140     150     160     170     180

           190     200     210     220
m667.pep  GADMYFILPPTHAARNRHNLMKMLHKKIAARLSTAFVLGNQHHL
           |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g667      GADMNLVLPFAHTAGNRHNLMDEVVLHKKIAAGLCAAFLLREQHHFVIRQGRQVIQRTDTL
           190     200     210     220     230     240

g667      HIGYGFNIESQNRHIGSTLHSKTDLRLCHX
           250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2181>:

```

a667.seq
1   ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51  TTTCCATTTC GTATTCGTCT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CGCAGATACA TCAGATAGGT ATTTACCGCA TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG CGTGAACGC CTCCACACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTCG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCGCTCG CCCATATCCC AATAGCGCGC GGCCTTGATG
401 CCGTGTAGCA GCGAACGGTA ATGCAGAACC GGCAGGTCGA AACCGCGCC
451 GTTCCAACCTG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCCTCG CCGTCATCCA TCTCGCGGAT TGTACCGACA
551 TGGACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAATCTG
601 ATGAAGATGA TGCTGCATAA AATCCCACCC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAAA CAGCACCCTG TCATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGAT TAAAA.CAG ACTTGCGCCT
801 ATTGTGTCAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2182; ORF 667.a>:

```

a667.pep
1   MRFVFLGGE IVSDPLDFHF VFVCVESAAD QTETQIHQIG IYRIGFAIIA
51  DFLQPARVER LPHLAHVHTQ LARKTAQFRH IVQRHIRPRL VKREIQIHQIA
101 MTLVVAADV VPLEIAAAVE IAVAHIPIAR GVDV*QRTV MQNRQVETAA
151 VPTDQLRRMF FNLEKFGDN HFLAVIHLAD CTDMDFILPP THAARNRHNH
201 MKMMLHKIPT RLSTAFLLGK QHHFIVGQRG RQVIQRTDTL HIGYGFNIES
251 QNRGHDSTLY LKXDLRLCH *

```

m667/a667 79.0% identity in 224 aa overlap

```

           10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPFDHFVFRVRIQPAADQTETQVHQISVCRVGFALLADFLQPARMEC
           ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a667      MRFVFLGGEIVSDPLDFHFVFVCVESAADQTETQIHQIGIYRIGFAIADFLQPARVER
           10      20      30      40      50      60

           70      80      90      100     110     120
m667.pep  LPNLAHVHTQLARKTAQFRHIVQRHVCPRLVKREIQIHQIAVALVITADVVPLEIAAAVE
           ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a667      LPHLAHVHTQLARKTAQFRHIVQRHIRPRLVKREIQIHQIAMTLVVAADVVPLEIAAAVE

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m667.pep	IAVAHIPIARGVDVAVYQGAVMQYGGIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD					
a667	IAVAHIPIARGVDVAVXQRTVMQNRQVETAAVPTDQLRRMFFNQLEKFGDNHFLAVIHLAD					
	130	140	150	160	170	180
	190	200	210	220		
m667.pep	GADMYFILPPHTHAARNRHNLMKMLLHKIAARLSTAFVLGNQHHL					
a667	CTDMDFILPPHTHAARNRHNLMKMLLHKIPTRLSTAFLLGKQHHFIVGQRGRQVIQRTDTL					
	190	200	210	220	230	240
a667	HIGYGFNIESQNRGHDSTLYLKXDLRLLLCHX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

```

g669.seq
1  ATGCGCCGCA TCGTTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

```

g669.pep
1  MRRIVKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```

m669.seq
1  ATGCGCCGCA TCATTAAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```

m669.pep
1  MRRIIKKHQP INAPHIVLEI RIMKLHRAFV FLGRKRPHHH DSSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	MRRIIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGI					
	EGMGFDFKQI					
g669	MRRIVKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGI					
	EGMGFDFKQI					
	10	20	30	40	50	60
	70	80	90	100		

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```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51 TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51 EGMGDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLLRRQHGI EGMGDFKQI
             |||||:|||||
a669        MRRIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGI EGMGDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGGTGAA
51 AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTGAGGTG
451 GGCTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGGTGAA
51 AAACGCTTCG GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTGCTCA AACACATTA

```


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```

251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTCAAGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              |||||
g670           FITFNTSPTISGSSAEVGSSNSITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX
              |||||
g670           SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAAGTCT CTGGCGCGT TCGTGTTCG GGTGGTAAA
 51 AAACGCTTCC GCGTTCGT CTTCGAGGAT TTGCCCTTA TCGACGAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 CCCGACCATT TCGGGGTCTGA GTGCGGAGGT CGGTCGTCA AACACATTA
251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTCAAGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

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```

              70      80      90      100      110      120
m670.pep    FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK
              |||||||
a670        FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK
              70      80      90      100      110      120

              130      140      150
m670.pep    SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
              |||||||
a670        SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX
              130      140      150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAAATG CGGTTGGCAA AGCCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAAACAgg cggggTTGGA ACGagGCAAA
201 GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTGTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAASLAK KKETTHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTTGGCAA AGCCCAAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAAACAGG CGGGGTTGGA ACGAGGCCAAA
201 GGCGAGGTCTG GCGAAGGAGG CGGCAAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep    MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
              |||||||
g671        MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep    RGWNEAKARSAKEAAKSLAKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL

```

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```

|||||
g671      RGWNEAKARSAKGAAKSLAKKKTTHATIEPASAITPRIVENTMQAAMTAEARRSAMGRL
              70      80      90      100      110      120

              130      140      149
m671.pep  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
|||||
g671      FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
              130      140

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2199>:

```

a671.seq
1   ATGACCAGCA GGGTAATAAT CAAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCCCCGG
101 TCAGCAGCGA GCGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA ACGATGCAAA
201 GCGGATGTCG GCGAAGGGTG CGGCAAAGAG TTTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGATGGCG GAGACGAGGA GGTCCGCAAC
351 GGGGAGGTTA TTCATTCGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAT  CGCGTTCGGC ATCCCTTGCG TTTTATAGT  TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2200; ORF 671.a>:

```

a671.pep
1   MTSRVIIKMP FNAPNTPPKM RLAKPKPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNDAKAMS AKGAAKSLAK KKATTHAAIE PASAITPRIA
101 DSTMQAAMMA ETRRSATGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

m671/a671 93.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
|||||
a671      MTSRVIIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep  RGWNEAKARSAKEAAKSLAKKKTTHAAIEPASAITPRIADSTMQAAMTAEARRSAMGRL
|||||
a671      RGWNDAKAMSAKGAAKSLAKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL
              70      80      90      100      110      120

              130      140      149
m671.pep  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
|||||
a671      FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
              130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2201>:

```

g672.seq
1   ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCG GCGCAGACGC ATTGGGACTG GTTTTATACC
101 CCCAAAGCCC CCGCGTATC GACATCATT AAGCACAAA AATCGCCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCAGGCGCA CGAAGACGAT GCATTCTGCC GGCAGTTCGA CCGCCCTAT
301 ATTAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC AACGCTCAGG CACTGCTGTT CGATGCCTAT CACCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGact GGacgctgtt ggcggAATAT
451 TCGGGCAAGC CGTGGGTGCT TGCCGCGCGG CTGACCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAAGC GGTGACGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```

g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATREF NAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKPAKVAAFI
201 ATANRLSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```

m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGCGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTCGATGTA TCCGGCGGTG
551 TGGAAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```

m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATREF DAQALLFDAY HPSEYGGTGN RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAKVAAFI
201 ATANRLSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICGITTTPEDAAAAAAGADAVGLVFFQSSRAVDIARAKKITAALPPFVSVVA					
	: : : : : : : : :					
g672	MRKIRTKICGITTTPEDALYAAHAGADALGLVFYQSPRAIDIKAQKIAAALPPFVSVVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m672.pep	LFVNESAQNIRRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATREF					
	: : : : : : : :					
g672	LFVNESAQNIRRILAEVPIHIIQFHGDEDDAFCRQFDRPYIKAIRVQTASDIRNAATREF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m672.pep	DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAESVDV					
	: : : : : : : : :					
g672	NAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAEAVDV					
	130	140	150	160	170	180
	190	200	209			
m672.pep	SGGVEASKGKKDAAKVAAFIATANRLSRX					
	: : : : : : :					
g672	SGGVEASKGKKDPAKVAAFIATANRLSRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

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```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCCG GCGCAGACGC ATTGGGACTG GTTTTACC
101 CCCAAAGCCC CCGCGCTGTC GACATCATT AAGCACAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCTAG CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GGCAGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
501 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTGATGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1  MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAV DIIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAAFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

```

              10      20      30      40      50      60
m672.pep  MRKIRTKICGITTPEDAAGADAVGLVFFQGSSRAVDIARAKKITAALPPFVSVVA
          |||||
a672      MRKIRTKICGITTPEDALYAAHAGADALGLVFYQSPRAVDIKAQKITAALPPFVSVVA
              10      20      30      40      50      60

              70      80      90      100     110     120
m672.pep  LFNESAQNIRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATREFP
          |||||
a672      LFNESAQNIRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRFP
              70      80      90      100     110     120

              130     140     150     160     170     180
m672.pep  DAQALLFDAYHPSEYGGTGNRFDWTLLEYSKGKPWVLGGGLTPENVGEAVRITGAESVDV
          |||||
a672      DAQALLFDAYHPSEYGGTGHFRFDWTLLEYSKGKPWVLGGGLTPENVDEAIRITGAEAVDV
              130     140     150     160     170     180

              190     200     209
m672.pep  SGGVEASKGKKDAKVAAFIATANRLSRX
          |||||
a672      SGGVEASKGKKDPAKVAAFIATANRLSRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCGC
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GGCGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG CGTACCGATG TATCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAACTCT TCCGCTATT

```

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```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAATAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAAGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CCGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          |||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK
          |||

```

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```

g673      YTDDTAQFVFDTPGFQTDHRNALNDRINQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
           70          80          90          100          110          120

           130          140          150          160          170          180
m673.pep  QLPKHTPVILVNVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130          140          150          160          170          180

           190          200          210          220          230          240
m673.pep  KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g673      KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190          200          210          220          230          240

           250          260          270          280          290          300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDNKVFLKVWVKVKS GWADDIR
           250          260          270          280          290          300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTGTGTTT GTCGATACGC CCGGTTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGGTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCCTTTGTT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRINQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFDT KVFVKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10          20          30          40          50          60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10          20          30          40          50          60

```

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	70	80	90	100	110	120
m673.pep	YTD	DDTAQFVFVD	TPGFQTDH	RNALNDR	LNQNVTE	ALGGVDVVVFVVEAMRFTDADRVVLK
a673	YTD	DDTAQFVFVD	TPGFQTDH	RNALNDR	LNQNVTE	ALGGVDVVVFVVEAMRFTDADRVVLK
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTP	VILVVKIDK	DKAKDRY	ALEAFVAQ	VRAEF	FAAAEAVSAKHGLRIANLLELI
a673	QLPKHTP	VILVVKIDK	DKAKDRY	ALEAFVAQ	VRAEF	FAAAEAVSAKHGLRIANLLELI
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPES	VPMYPED	MVTDKS	ARFLAME	IVREKL	FRYLGEELPYAMNVEVEQFEEDGLNR
a673	KPYLPES	VPMYPED	MVTDKS	ARFLAME	IVREKL	FRYLGEELPYAMNVEVEQFEEDGLNR
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVL	VDKESQ	KAILIG	KGGERL	KKISTE	ARLDMEKLFDTKVFLKVWVKVSGWADDIR
a673	IYIAVL	VDKESQ	KAILIG	KGGERL	KKISTE	ARLDMEKLFDTKVFLKVWVKVSGWADDIR
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETYPY
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCAGAG TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```


51 FFGTQTNAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	::					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAAACAG	CCGCCGCGC	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCGAAAC	GCCCTACCCC
301	GTCATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACGCGCC	GCCCAAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcacgctc
151 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAAC TTGC
201 CTCTTCCGAA AAATTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCTRLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
 101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAKVAV ECANLVNLLL
 151 EEQFEDEE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq
 1 ATGAACACCA TCGCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
 201 CTCTTCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
 251 GCGAAACCTA CCATTTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
 301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
 351 CACCGAAAAC GACGCGCAGG CAATCGAAGC GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCGGTC GAATGCGCCA ACCTCGTCAA CCGTCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV
 101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL
 151 EEQFEDEE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCTRLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFEVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFEVSNESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq
 1 ATGAACACCA TCGCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
 201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
 251 GCGAAACCTA CCATTTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
 301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
 351 CACGGAAC GACGCACAGG CAATCGAAGC GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCGGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV

1085

```

101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL
151 EEQFEDEE*

m675/a675    100.0% identity in 158 aa overlap

              10      20      30      40      50      60
m675.pep     MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP
              |||||
a675          MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP
              10      20      30      40      50      60

              70      80      90      100     110     120
m675.pep     IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN
              |||||
a675          IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN
              70      80      90      100     110     120

              130     140     150     159
m675.pep     DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX
              |||||
a675          DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX
              130     140     150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

```

g677.seq
1  ATGCCGCAGA TTTTGGTGCG GATTTCCTC ATTCGGTATT CCTTTATTg
51  ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCCGGCGT
151 GTTCAAAACC ACTTCGTGCG CTTGCGCGCG TTTAATCAGG CAACGCGCCA
201 ACGGCGAAAT CCAAGAAATT TTGTTTGCG CGGTATCGAT TTCATCGACG
251 CCGACGATT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTGCGCGCG AAAAATACTT GGTGCGTCG TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTG
401 ATTCGCGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGT TTTGCTGCG
451 GTCGCCGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGTAATGT AGTTTGTGGT TTCGTACTC ATATTGTGTG CGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

```

g677.pep
1  MPQILVRIFL IRYFSIWETV RLCRFRHSR SVDFDVDRK DFNFLTAFR
51  VQNHFAFAR FNQATRRRN PRNFVLRGID FIDADDFDGL LAPVAAQOTD
101 GRAEKLVRG FAQFGIDDDG SLQTFGOETD AAVDFAHAF AVKIVAVFAA
151 VAVACRPVDD LDDEGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

```

m677.seq
1  ATGCCGCAGA TTTTGGTGCG GATTTCCTC ATTCGGTATT CCTTTATTG
51  GGAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCCGGCGT
151 GTTCAAAACC ACTTCGTGCG CTTGCGCGCG TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTGCG CGGTATCGAT TTCATCGATG
251 CCGACGATT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCGAC
301 CGTCGCGCG AAAAACAATT GGTGCGTCG TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTG
401 ATTCGCGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGT TTTGCTGCG
451 GTCGCCGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTGTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGTAATGT AGTTTGTGGT TTCGTACTC ATATTGTGTG CGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

```

m677.pep
1  MPQILVRIFL IRYFSIWETA RLCRFRHSR SVDFDVDRK DFNFLTPFR

```

1086

```

51  VQNHVFARFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHATF AVKIVAVFAA
151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

```

              10      20      30      40      50      60
m677.pep      MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDKDFNFLTFFRRVQNHVFARFAR
              |||||
g677           MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVFDKDFNFLTAFRRVQNHVFARFAR
              10      20      30      40      50      60

              70      80      90      100     110     120
m677.pep      FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
              |||:|
g677           FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGGRAEKYLVRFAQFGIDDDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m677.pep      SLQTFGQETDAAVDFAHATFAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
              |||||
g677           SLQTFGQETDAAVDFAHATFAVKIVAVFAAVAVACRPVDDLDDFGAFFIDQLIKLVFQCL
              130     140     150     160     170     180

              190     199
m677.pep      PSGGRNVVFGFGTHIVCGX
              |||||
g677           PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

```

a677.seq
1  ATGCCGCGAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
51  GGAAACGGCG CGTTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTCAATT TCCTCACGCC CTTCGGGCGT
151 GTTTAAACC ACTTCGTCGC CTTACGCGC TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTTCGC CGGTATCGAT TTCATCGATG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTCGCGCCG AAAAACACTT GGTCGGTCGC TTCGCGCAAT TCGGGATCAA
351 CGACGACGGC GGCTTCCAAA CGCTTGGTCA GGAAACGGAT GCGGCGGTTCG
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGG TAGTCGCCGT TTTGCTGCG
451 GTCGCGGTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTAAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CCGATGA

```

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

```

a677.pep
1  MPQILVRIFL IRYFSIWETA RLRCFRHRSR SVDFDVFDK DFNFLTFFRR
51  V*NHFVAFTR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVAAQQTD
101 GRAEKHLVGR FAQFGINDDG GFQTLGQETD AAVDFAHATF AVKVVAVFAA
151 VAVACRPVDD LDDFGAFFIN QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

m677/a677 93.4% identity in 198 aa overlap

```

              10      20      30      40      50      60
m677.pep      MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDKDFNFLTFFRRVQNHVFARFAR
              |||||
a677           MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDKDFNFLTFFRRVXNHVAFTR
              10      20      30      40      50      60

              70      80      90      100     110     120

```

1087

```

m677.pep  FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRRAEKHLVGRFAQFGIDDDG
a677       FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQTDGRAEKHLVGRFAQFGINDDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m677.pep  SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFVDQLIKLVFQCL
a677       GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFINQLIKLVFQCL
              130     140     150     160     170     180

              190     199
m677.pep  PSGGRNVVFGFGTHIVCGX
a677       PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
51 CTGCATCGTC ATTTCCACGA TGC CGCGCGT GATTGCGGAA GCaggttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTtg ccAAACTCTt tGCCGCACcc
151 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCATTc ATTTCCCTGT TCGTCATTGC CTGCTGATC CAGAAAATGC
251 TCCGTTGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATT TGGGCGGTGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC ataccgaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGC CGCGCGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCTT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCC GCCTGT TTGCATTGGC
201 TCTGTGCTTc ATTTCCCTGT TCGTCATTGC CTGCTGATC CAGAAAATGC
251 TCCGTTGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATT TGGGCGCGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLP	ADLLV	SAVIA	ACIVL	SAMRG	VIAEAGS
	MAAVV	VSFFF	AKLFA	ASFAD	LAFAS	FQ
	:	:	:	:	:	:
g678	MNSLP	ADLLA	SAVIA	ACIVL	ISTMR	GVIAE
	AGSMV	AWVVS	FFF	AKLFA	APFAD	LAFAS
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLF	ALALS	FISLF	VIACLI	QKMLR	SLLTS
	AVS	AVGLG	FANRIL	GGVFG	ALKGV	LIVTLL
	:	:	:	:	:	:
g678	PRLF	ALALS	FISLF	VIACLI	QKMLR	SLLTG
	AVS	AVGLG	FANRIL	GGVFG	ALKGV	LIVTLL
	:	:	:	:	:	:
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLAS	KTDLP	DTTEW	RQSYTL	PFVSL	SEAVLN
	HSGGT	AETPE	DDX			
	:	:	:	:	:	:
g678	IMLAS	KTDLP	DTTEW	QSYTV	PFVSL	SEAVLN
	HNTDN	APESL	DDX			
	:	:	:	:	:	:
	130	140	150	160		

a678.seq

```
1  ATGAATAACC TCCCGGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TGC GCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTT TTTTCG CCAAAC TCTT TGCCGCACCC
151 TTCGCCGACA TCGCCTTTGC ATCGTCCAA CCCCCTGTG TTGCATTGGC
201 TCTGTCTGTC ATTTCCCTAT TCGTCATTGC CTGTCTGTAT CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTGCGTTT GGGCTTTGCC
301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCTGCTG GTCATGCTCG CTTCAAAAC CGACCTGCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCA
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGGAA ACGATTAGC
```

a678.pep

1	MNNLPVADLL	VS	AI	AACIV	LS	AMRGVIAE	AG	SMAAWVVA	FF	FAKLFAAP
51	FADIAFASFQ	PR	LF	ALALSF	IS	LFVIACLI	QK	ILRSLITG	AV	SAVGLGFA
101	NRILGGVFGA	LK	GILITLL	VML	ASKTDLP	DTE	EW	RQSYT	LP	FFVSLSEA
151	VLNHSGGTAE	TP	EDD*							

	10	20	30	40	50	60
m678.pep	MNSLP	ADLLVS	AVIAAC	IVLSAM	RGVIAE	AGSMAA
	WVVSF	FFFAKL	FAASF	ADLAF	ASFQ	
a678	MNNLP	VDLLVS	AIACIV	LSAMRG	VIAEAG	SMAAWV
	VVVAFF	FAKLFA	APFAD	IAFAS	FQ	
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLF	ALALSF	ISLFV	IACLIQ	KMLRSL	LTSAVS
	AVGLG	FANRIL	GGVFG	ALKGV	LIVTLL	
a678	PRLF	ALALSF	ISLFV	IACLIQ	KILRSL	LTGAVS
	AVGLG	FANRIL	GGVFG	ALKGIL	IITLL	
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLAS	KTDLPD	TEEWRQ	SYTL	PFFVSL	SEAVLN
	HSGGTA	ETPEDD	X			
a678	VMLAS	KTDLPD	TEEWRQ	SYTL	PFFVSL	SEAVLN
	HSGGTA	ETPEDD	X			
	130	140	150	160		

g680.seq

```
1 ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51 GGCGACGAGG ACGCGCAGGC TGCCTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
```

1089

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCTG
451 TCGATAAAC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTAAACTGA TGTTTTCTG TTTACATGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACT ATTTCGCAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
51 GCGGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGCGC GCGGACTTCG ACGGTTTCGG GCGGTTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCTG
451 TCGATAAAC CCATATCCAG CACACGGTCG GCTTCGTCCA AAACGACGAT
501 TCGACTTTG TTCAAATGGA TGTTTTCTG TTTACGTGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACG ATTTCGCAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPKN TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||||
g680      MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep TLCLVLQNTMTWFICKSTISRSSRLRFKXMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||||
g680      TLCLVLQKTI TWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

```


1090

```

|||||
g680      ASLRIGA EKVAEKSRVWRWRG SICMILRMSSINPISNMRSASSRTTISALEFKLMFFCFTW
          130      140      150      160      170      180

          190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRT VCRSGRFLMX
          190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```

a680.seq
1  ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCC GCGCGG CGATATCGGT
51  GGCGACGAGG ACGCGCAGGT TGCCGCTCTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTG CACGCTTTGT TGGTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAATC GACAATCAGC CGTTCGAGCA
251 GGTTGCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTCTTGCGC GCGCACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTGC
451 TCGATAAAAC CCATATCCAG CATA CGGTGCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTGG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GCGGACGACG ATTTTCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTTCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```

a680.pep
1  MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGA EKVAEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPNKT TVWRSGRFLM *

```

m680/a680 98.6% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||||
a680      MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRFKXMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||||
a680      TLCLVLQNTMTWFICKSTISRSSRLRFKXMVSTAMMCCSTLALVVSCAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGA EKVAEKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
          |||||
a680      ASLRIGA EKVAEKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
          130     140     150     160     170     180

          190     200     210     220
m680.pep  SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          |||||
a680      SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

```

g681.seq
1  ATGACGACGC CGATGGCAAT CAGTGGCTCA AATTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAGCGC GCCGGGTACG GTGGcgacgg

```

1091

```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTG GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCCgt cgaggttgGG GGCATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GTCGTCGGT
451  GTATTCCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTGTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTCCCGCGT TGTGCGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCGCC GTTTCAGGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

g681.pep
1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGNGLGEC AVFGKLPRAA FGLGKQCGGF RVFGDVGVEA DDAEVVGVVG
151 VFVGFVAEE TPAAVVFKNG GFAVKEADGP VLFGDVGVEA AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCGTCA AACTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTG CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GGCATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCGGT
451 GTATTCCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGATTTT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAG
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLEC AVFGKLPCAA FGLGEQCGGF RVFGDVGVEA DDAEVVRIIVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGP VLFGDVGVEA TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          |||||
g681      MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVG DGLECAVFGKLPCAA					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGNGLECAVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDVGEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
g681	FGLGKQCGGFRVGFVDVGEADDAEVVGVGVFVGFVAAEETPAAVVFKNGGFAVKEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
g681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGLADFTTIIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKRIRAVFCGRRX					
g681	LRCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1  ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTC GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGGATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTGCTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTT. GGGGAAAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1  IITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
a681	IITPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVG DGLECAVFGKLPCAA					
a681	KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVG DGLECAVFCQFPRAA					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKNGGFAVEE	ADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKNGGFAVEE	ADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHYGN	TLGXKLTDFTTIRAL	SADGGGLVVQCAPFAAL		
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHCGNT	XGGKLADFTTILALSAD	GGGLVVQCAPFAAL		
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIRAV	FCGRRX				
a681	RCFCIFGVWKRIRAV	FCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAT GCCGCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTG
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTC AACTGACCGA
301 CCCATTTCGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVS YGKWRKNWDIR YCLLHLIHL STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. EMAMPSEP DWIQTAFCM YGFIRFPTDR
101 PIRTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||:|||||:||||| |||:|| ||||| ||||| ||||| ||||| ||||| |||||
g682      MRDFAVWVPYGERRKNWDIRYCLPHLIRLSPTLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY-----EMAMPSEPDWIIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR
          ||||| |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      PILILIDYICVNDEIKMPSEPDWIIQTAFDMA-GFIRFPTDRPILTRQSGVVRISPRTGFR
          70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      YPTRSLPKSKKAYGX
          120     130

```

```

a682.seq
  1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCACCCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGCTCG
151 ATTACGCCCG ATTTGACGAT GCATACTGTG CCTATTTTGA TTTTAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATCTCGA CAAGGCCGAC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

```
a682.pep
  1 MRDFTVWVSY GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
51 ITPDLTMHYC PILILIEY.. ..... ..YIRFPTDR
101 PILTRPTGVV RISPRTGFRY PTRSLPKSKK AYG*
```

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||||
a682      MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||||

      70      80      90      100     110     120
m682.pep  PILILIDYEMAMPSEPDWIIQTAFCMAYGFIRFPTDRPIRTQSGVVRISPERTGFRYPTRS
          |||||:|:||||||| ||:|||||||
a682      PILILIEY-----YIRFPTDRPILTRPTGVVRISPERTGFRYPTRS
                          70      80      90      100

      130
m682.pep  LPKSKKAYGX
          |||||
a682      LPKSKKAYGX
          |||||
      110

```

g683.seq

1	ATGATTAAGG	AAACCCTAAT	GCGCCCAATC	TTCCTATCTT	TCGTTTTACT
51	CCCTATTTTG	ATAACCGCCT	GCAGCACACC	GGACAAGTCT	GCCCGATGGG
101	AAAATATCGG	CACAATCTCA	AACGGCAATA	TTCATACATA	TATTAATAAA
151	GACAGTGTGA	GAAAAAACGG	AAATCTGATG	ATTTTCCAAAG	ATAAAAAAGT
201	TGTTACCAAT	CTGAAACAAG	AACGTTTTCG	CAACACCCCC	GCATAAAGA
251	CTGCCATTGC	CGAGTGGGAA	ATCCACTGCA	ACAACAAAC	ATACCGCTTA
301	AGTTCGCTAC	AGTTATTTGA	TACAAAAAC	ACGGAAATT	CCGACAAAA
351	CTACACAGCC	TTTCCCTCC	GCCCGATGAG	CATCCTGTCC	GGGACATTAA

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

g683.pap

1 MIKETLMRPI FLSEVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTACCAAT CTAAAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pap..

1 MIKETLMRPI FLSEVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pap	MIKETLMRPIFLSEVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSEVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
m683.pap	70	80	90	100	110	120
	IFQDKKVVVN LKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVVN LKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
m683.pap	130	140				
	SSLRPMSILSGTLTEKQYETVCGKKLX					
g683	SSLRPMSILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTACCAAT CTAAAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pap

1 MIKETLMRPI FLSEVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

```

      10      20      30      40      50      60
m683.pep  MIKETLMRPILSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
          |||||
a683      MIKETLMRPILSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
          |||||
      10      20      30      40      50      60

      70      80      90     100     110     120
m683.pep  IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
          |||||
a683      IFQDKKVVTNLKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA
          |||||
      70      80      90     100     110     120

      130     140
m683.pep  SSLRPMISLSGTLTEKQYETVCGKKLX
          |||||
a683      SSLRPMISLSGTLTEKQYETVCGKKLX
          |||||
      130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

```

1  ATGCGCCTTT TCCCCATCGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACCGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCATCAACAC
201 CGCACAAAAC CATGTTTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGACA GCACACGCAC CTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGACAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

```

1  MRLFPIAAL TLAACGTVQS TQYFVLPDSR YIRPATQGE TAVEVRLAEP
51  LKRGGLVYQT DRYRINTAQN HWADTLDDM LEAALNAFN RLDSTRTFVP
101 ASRSGSTDKW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD
151 GYAAMTALE QGLKQAAQM VE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

```

1  ATGCGCCTTT TCCCGATTGC CGCCGCCCTG TCGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACTGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CACGTCTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGACA GCACACGCAT CTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGAAAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CGATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

```

1  MRLFPIAAL SLAACGTVQS TQYFVLPDSR YIRPATQGE TAVEVRLAEP
51  LKRGGLVYQT DRYRLNTAQN HWADTLDDM LEAALNAFN RLDSTRIFVP
101 ASRSGSTEXW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD

```

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m684.pep	MRLFP	IAAALS	LAACTG	VQSTQY	FVLPS	SRYIRPATQGGETAVEVRLAEPLKRGGLVYQT
g684	MRLFP	IAAALT	LAACTG	VQSTQY	FVLPS	SRYIRPATQGGETAVEVRLAEPLKRGGLVYQT
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLN	TQAQN	HVWADT	LDLDM	LEAALS	NAFNRDSTRIFVPASRSGSTEKWTVVYIDAFQGS
	:					
g684	DPYRINT	AQAQN	HVWADT	LDLDM	LEAALS	NAFNRDSTRITFVPASRSGSTDKWTVVYIDAFQGS
	70	80	90	100	110	120
	130	140	150	160	170	
m684.pep	YTGKT	LISGYAV	LPDGTNR	PFHIETEQ	QGDGYAAMTAAL	EQGLKQAQQMVEX
g684	YTGKT	LISGYAV	LPDGTNR	PFHIETEQ	QGDGYAAMTAAL	EQGLKQAQQMVEX
	130	140	150	160	170	

```
a684.seq
1 ATGCGCCTCT TCCCGATTGC CGCGCGCCTG ACGCTTGCCG CCTGCGGTAC
51 TGTGCAAAAG ACACAATATT TCTGTTGTGC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGCGCGCGAA AACTGCCGTC AAGTCCGCTG TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCCTAACAC
201 CGCACAACAA CACGTCCTGG GACAGACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGACA GCACACGATG CTTTGTCTCT
301 GCCTCACGCA CGGGCAGTAC CGAAAATGG ACGGCTCTATA TCGACGCTAT
351 CCAAGGCAGC TACACGGGCA AAACCTCAT CAGCGGCTAC GCCGTCCTAC
401 CGCAGGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCATCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG TCTGAGTAA
```

a684.pap

1	MRLFPAAAL	TAAAGTVQS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAAL	QGLKQAAQOM	VE*		

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

	10	20	30	40	50	60
m684.pep	MRLFP	IAAALS	LAACGT	VQSTQY	FVL	PDPSRYIRPATQGGETA
a684	MRLFP	IAAALT	LAACGT	VQSTQY	FVL	PDPSRYIRPATQGGETA
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRL	NTAQN	HVWADT	LDDMLE	AALS	SNAFNRLDSTRIFVPASRSGST
a684	DPYRL	NTAQN	HVWADT	LDDMLE	AALS	SNAFNRLDSTRIFVPASRSGST
	70	80	90	100	110	120
	130	140	150	160	170	


```

m684.pep      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQMVEX
              |||||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQMVEX
              130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TCGGGCGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCAC
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCCGGCCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAACT GTATccgCCG CATCCCAAGC
201 CGCATCCACA CCTGTCGCCA CGCTGACCGT GCGGACCGCG CGGGCGGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgtcg ccgtgtAcga CtggCGGCGC
301 TtggATACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTCG AGCCTGCATT TGACAAGGCG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TGCGAATCCC TGCACCGCCA CAATCCGAG
451 TTTGTCATTA CCGGCGGGCC GGTGCGGAA GCGTATGAAC AGTTGGCGAA
501 AAACGCGACC ACCATAGATT TGACGGTGA CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTTCGG TAAGGAAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTTCG CCAAAAGCG
651 CGAAGCCGCG AAAGGCAAAG GACGCGGGCT GGTGCTGTCG GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGGCAAG TTGGATACAC
751 GCGGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGCA
801 CGGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTATCATAT CGACCGCACC GCGCCATCGC GGCAGGAAG GCGCGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGCGGCG GTTTGAAAAG
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685 >:

```

g685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEPAEKT VSAASQAAS PVATLTVPPTA RGDVAVPKNP ERVAVYDWA
101 LDTLTPGVN VGATTAPVRV DYLPAPFKA ATVTGLFEPD CESLHRHNPQ
151 FVITGGPGE AYEQLAKNAT TIDLTVDNGN IRTSGEKQME TLSRIFGKEA
201 RVAELNAQID ALFAQKREA KGKGRGLVLS VTGNKVSAGF TQSRLASWIH
251 GDIGLPPVDE SLRNEGHHGP VSFEYIKEKN PGWIFIIDRT AAIQOEGPAA
301 VEVLDNALVC GTNAWKRKQI IVMPAANYIV AGGARQLIQA AEQLKAAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

m685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TCGGGCGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCAC
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAACT GTATCCGCGC CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TCGCGGTGGA
351 TTATTTCGAG CCTGCATTTC ACAAGGCGGC AACGGTGGGG ACGCTGTTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGGGGCGCG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGACTCG ACGGTGGACA ACGGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAGGA CGCGGGCTGG TGCTGTGCGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGCG
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAAGT ACATTGTGCG GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGCG GGAGCAGTTG AAGGCGGCGT TAAAAAGGC AGAACCCGTT
1051 GCGCGGCGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685.pep

1099

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAEAKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPAGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESRLN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30      40      50      60
m685.pep      LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAEAKT
              |||
g685           LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPPEPAEAKT
              10      20      30      40      50      60

              70      80      90      100     110
m685.pep      VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
              |||
g685           VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV
              70      80      90      100     110     120

              120     130     140     150     160     170
m685.pep      DYQLQPAFDKAATVGTLEFPDYEALHRYNPQLVITGGPGAAYEQLAKNATTIDLTVDNGN
              |||
g685           DYQLQPAFDKAATVGTLEFPDCESLHRHNPQFVITGGPGAAYEQLAKNATTIDLTVDNGN
              130     140     150     160     170     180

              180     190     200     210     220     230
m685.pep      IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKRGVLVSVTGNKVSAGF
              |||
g685           IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGKRGVLVSVTGNKVSAGF
              190     200     210     220     230     240

              240     250     260     270     280     290
m685.pep      TQSRLASWIHGDIGLPPVDESRLNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
              |||
g685           TQSRLASWIHGDIGLPPVDESRLNEGHGQPVSEFYIKEKNPGWIFIIDRTAAIGQEGPAA
              250     260     270     280     290     300

              300     310     320     330     340     350
m685.pep      VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAAGKKX
              |||
g685           VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTTGCC GTATCGGGAA TTTTGCCTTT TGC GCGCTGG TTTCTGCAGG
51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGGCTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGC GCGTGA
351 TTATTTGCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCC
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGGGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAAGG CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCGG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAGCGCA AGCAAATCAT
951 CGTCATGCGT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
  1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
 51  CSPEPAEAKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101  TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151  GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201  LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAFGTQSR LASWINGDIG
251  LPPVDES LRN EGHGQPVSE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301  DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQ KEAFKAEPV
351  AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

m685/a685 98.9% identity in 355 aa overlap

m685.pep	10	20	30	40	50	60
a685	10	20	30	40	50	60
m685.pep	70	80	90	100	110	120
a685	70	80	90	100	110	120
m685.pep	130	140	150	160	170	180
a685	130	140	150	160	170	180
m685.pep	190	200	210	220	230	240
a685	190	200	210	220	230	240
m685.pep	250	260	270	280	290	300
a685	250	260	270	280	290	300
m685.pep	310	320	330	340	350	
a685	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

```

g686.seq (partial)
  1  ..AATTCCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
 51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101  GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCCTCAGCA TAGCGCCGGC
151  ATTGTGGAAG CCGTCGGCAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201  GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251  TCCTTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301  GCCGTCGGCG GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351  TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)
 1 ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
 51 IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
 101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..
 1 ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTGGC
 51 GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
 101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
 151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGCTG TATCGGGTGG
 201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGCG TCAGCATACT ACCGGCATTG
 251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
 301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
 351 TCGCCGCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
 401 TCGGCGGGAT GGTGTTTCGTA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
 451 TCCGTCAACG GGAATACCG CTTCATCAGA ATCGGAATGT GA

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep
 1 MMLKKFVLGG IAALVLAACG GSEGGSGAXX XNMFSCSADD VFNDICSAVE
 51 GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
 101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
 151 SVNGTTGFIR IGM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACGGSEGGSGAXX	XXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG				
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFVRIGMX				
m686		GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFIRIGMX				
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)
 1 ..AATTCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT
 51 TGAAGCTTC GCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
 101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACGGT
 151 ATTGTGGAAG CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
 201 GGTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
 251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
 301 GCCGTCGCGC GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC
 351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

```

      10      20      30      40      50      60
m686.pep  LKKFVLGGIAALVLAACGGSEGGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
      |||  ||||:|||||:|||||
a686      NFSCRADDVFDDICSAVESFGGIARSVQLG
      10      20      30

      70      80      90      100     110     120
m686.pep  AVSGGAFESVAYSRLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
      |||  |||||  |||||  |||||  |||||  |||||
a686      AVSGGAFESVAYSRLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
      40      50      60      70      80      90

      130     140     150     160
m686.pep  GIAAALWPVIAVGGMVFVSVPMDDAVKAKSVNGTTGFIRIGMX
      |||  |||||  |||||  |||||  |||||  |||||
a686      GIAAALWPVIAVGGMVFVSVPMDDAVKAESVNGTTGFIRIGMX
      100     110     120     130

```

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g687.seq
1  ATGAAATCCA  GACACCTCGC  CCTCGCCCTC  GGCCTTGCCG  CCCTGTTCGC
51  CTTTGGCGCG  TGGCAGACGA  AAGTGCAAAC  CAGCGTCCCC  CGCAGAGCGG
101 CGCCTGCCGC  TTGGCGAGCC  GCCGCCCCGG  CAGCACTGGT  GCGACAGCA
151  AACTACACCG  TCCTTGCCAA  CCGGATTCCC  CAACAGCAGG  CAGGCAAGGT
201  TGAAGTGCTT  GAGTTTTTCG  GCTATTTTTG  TCCGCATCGC  GATCCCTCTg
251  AACCTGTTTT  GACCAACAC  CCAAGTCTT  TTAAGACGA  TATGTACCTT
301  CGTACCGAAC  ACGTCGCTG  GCAGAGGAA  ATGCTGCCGC  TGGCAGCGCt
351  cGCCGCCCGC  TCGATATGG  CTGCCCGCGA  AAGCAAGAT  GTGGCGAACa
401  GCCATATTTT  CGATGCGATG  GTCACCAACA  AAATCAAGCT  GCAAGAGCCG
451  GAAGTCTCTA  AAAAATGGCT  GGGCGAACa  ACggcctTTG  ACGGCAAAAA
501  AGTCCTTTGC  GCCTACGAAT  CCCCCGAAAG  TCAGCGCCGC  CGcggaAAAA
551  TGCAGGAGCT  GACCGAAACC  TTCCAATTCG  ACGGTAGCCG  CACGGTTATC
601  GTCGGCGGCA  AATATAAAGT  CGAATTTGCC  GACTGGGAGT  CCGGTATGAA
651  CACCATCGAC  CTTTGTGGCG  ACAAAGTACG  TGAAGACAA  AAAGCCCGCG
701  AGTAG

```

g687.pap

1	MKSRHLALAL	GVAALFALAA	CDSKVQTSVP	ADSAPAASAA	AAPAGLVEGO
51	NYTVLNLNPI	QQAGKVEVL	EFFGYFCFHC	ARLEPVLSKH	AKSKDDMYL
101	RTEHVWVQKE	MLPLARLAAA	VDMAAESKD	VANSHIFDAM	VNQIKLQEP
151	EVLKKWLGEQ	TAFDGKKVLA	AYESPESQAR	AKGMQELTET	FQIDGTPTVI
201	VGGIKVVEFA	DWESGMTTID	LLADKVRREEQ	GAAG*	

```
m687.seq
1  ATGAAATCCA GACACCTTGC CCTCgGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGGCAG AGCAAAGTCC AAACCAGCGT CCCGCCGCAG AGCCGCGCTG
101 CGGCTTCGGC AGCCGCGGCC CGCGCAGGGC TGGTCGAAGG GCAAAACTAT
151 ACCGTCCTTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCCACT CTCGAACCTG
251 TTTTAAGCAA ACGCGCAAG TC7TTTAAAG ACGATATGTA CCTCGGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCTTCGCCGC
351 CGCGCTCGAT ATGGGTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGTGCAAC AAAAAATCAA AGCTGCAAAA TCCGGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAAACGCC TTTGACGGCA AAAAAGTCCT
```

```
m687.pep
1   MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVGEQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TIALRLAAVD MAAADSKDVA NSHIFDAMVN QKIRLQNPEV
151 LKKWLGEQTA FSGKKVLAAY DESPEQRQA KMQLTETTFQ IDGPTFTVVG
201 GKYKVEFADW EGMNTIDLL ADKVREEQKA AQ*
```

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

		10	20	30	40	50	
m687.pep	MKSRHLAL	--GVAALFALAACDSKVQTSVPADSAPAASAAAA	PAGLVEGQNYTVLANP	IP			
g687	MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAA	PAGLVEGQNYTVLANP	IP				
		10	20	30	40	50	60
m687.pep		60	70	80	90	100	110
	QQQAGKVEVLEFFGYFCPHCAHLEPVL	SKHAKSFKDDMYLRTEHV	VWQKEMLT	LARLAAA			
g687	QQQAGKVEVLEFFGYFCPHCARLEPVL	SKHAKSFKDDMYLRTEHV	VWQKEML	PLARLAAA			
		70	80	90	100	110	120
m687.pep		120	130	140	150	160	170
	VDMAAADSKDVANSHIFDAMVNQKIKL	QNEPVLKKWLGEQ	TA	FDGKKVLAAYES	PESQAR		
g687	VDMAAAESKDVANSHIFDAMVNQKIKL	QNEPVLKKWLGEQ	TA	FDGKKVLAAYES	PESQAR		
		130	140	150	160	170	180
m687.pep		180	190	200	210	220	230
	ADKMQELTET	FQIDGTP	TVIVGGK	YKVEFADWESGMNT	IDLLADK	VREEQKAAQX	
g687	AGKMQELTET	FQIDGTP	TVIVGGK	YKVEFADWESGMNT	IDLLADK	VREEQKAAQX	
		190	200	210	220	230	

```

a687.seq
1      ATGAATATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
51     CGCGTGGCAGC AGCAAAGTCC AAACACAGCGT CCGCGCGGAC AGCGGCGCTG
101    CCGCTTCGGC  AGCCGCCGCC CCGGCAGGCG TGGTCGAAGG GCAAAACTAT
151    ACTGTCTCTTG CCAACCCGAT TCCCTCAACG CAGGCAGGCA AATGTCAAGT
201    CCTTGAATTT  TCTGGCTATT TCTGTCCGCA CTGCGCCCA  CTGGAACCTG
251    TTTTAAGCAA  ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301    GAACACGCTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCGCTCGCGC
351    CGCCGTCGAT  GCGCTGCGC  CGACAGCAA  AGATGTGGCG AACAGCCATA
401    TTTTCGATGC  GATGGTCAAC CAAAAATCA  AGCTGCAAGA GCCGGAAGTC
451    CTCAAAAAAT  GAATGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCTT
501    TGC CGCTTAC  GGCTCTCCG  AAAGCAGGCG CGCGCGCGAC AAAATGCAAG
551    AGCTGACCGA  AACCTTCCAA ATCGACGGTA CGCCACGGT  TATCGTCGGC
601    GGC AAATATA  AAGTCGAAT  TGCCGACTGG GAGTCCGGTA TGAACACCAT
651    CGACCTTTTG  CGGCACAAG  TACCGCAAGA ACAAAAAGCC CGCACTAA

```

a687.pep

1	MKS KHLALGV	AALFALAACD	SKVQTSVPAD	SAPAAASAAA	PAGLVEGQNY
51	TVLANPI PQQ	QAGKVEVLEF	FGYFCPCAH	LEPVLKHKAK	SFKDDMYLR
101	EHV VWQKEML	TLARLAAAVD	MAAADSKDVA	NSHIFDAMVN	QKIKLQEPEV
151	LKKWLGEQTA	FSGKRVLAAY	ESPEAQARD	KMQLETTFQ	IDGTPTVIVG
201	GKYKVEFADW	EDGMNTIDLL	ADKVREOKA	KH*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

	10	20	30	40	50	60
m687.pep	MKSRHLALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSKHLALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m687.pep	QAGKVEVLEFFGYFCPHCAHLEPVLKSHAKSFKDDMYLRTEHVWVQKEMLTARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLKSHAKSFKDDMYLRTEHVWVQKEMLTARLAAAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m687.pep	MAAADSKDVANSHIFDAMVNQIKLQNEVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKLQNEVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m687.pep	KMQELTETFDIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX					
a687	KMQELTETFDIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTGACACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCTCATC	CTCGCCCTTT	CGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAT	CATCCAAGGC
151	AACGAACCTG	AACCGCGCGC	CGTTGCCGCC	CTGCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688>:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAAEAL	RAKQNADKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTGACACAG	AAAGGCATT	CCGTGAACAA
51	AACCTCATC	CTCGCCCTTT	CGCCCTCCT	CGGCCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCCTGTTC	CCCTCGTACA	AACTCAAAT	CATACAGGGC
151	AACGAACCTG	AACCGCGCGC	CGTTGCCGCC	CTCCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGTCCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAAEAL	KDRQNTDKP*	

Homology with a predicted ORF from *N. gonorrhoeae*

m688/g688 90.6% identity in 138 aa overlap

		10	20	30	40	50	60
m688.pep		VLHYPSRFAQKGISVNKTLILALSALLGLAACSAERVS	LFP	SYKLKII	QGN	LEPR	AA
g688		VLHXTSRFAQKGSPVNKTLILALSALFSLTACSV	ERV	S	LFP	SYKLKII	QGN
		10	20	30	40	50	60
		70	80	90	100	110	120
m688.pep		LRPGMTKDQVLLLLGSPILRDAFH	TD	RWDY	TFNTSR	NGIIKERS	N
g688		LRPGMTKDQVLLLLGSPILRDAFH	TD	RWDY	TFNTSR	NGIIKERS	N
		70	80	90	100	110	120
		130	140				
m688.pep		DVLQNAAEAL	KDRQNTDKPX				
g688		DALQNAAEAL	RAKQNADKQX				
		130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2289>

```
a688.seq
1 GTGTTACACT ACCCATCCCG ATTGCACAG AAAGGCATT CCGTGAACAA
51 AACCCTCATC CTCGCCCTTT CGGCCCTCCT CGGCCTTGCC CCGTGCACGC
101 TCGAACGCGT TTCACGTGTT CCTCGTACA AACTCAAAAT CATACAGGCG
151 AAGCAACTCG AACCTCGCGC CGTCGCGCTC CTCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTCGCG CAGGCATATCC
251 ATACCGACCG CTGGGACTAT ACCTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAACGCGC TGCTCGTCCG
351 CACCGAAGCG AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGACGA CAACCAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

a688.pap

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSVERVSIF	PSYCLKIIQG
51	NELEPRAVAS	LRPGMTKDQV	LLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KDRSNLTVVF	ENGVLVRTEG	NALQNAAEAL	RVKONAKDO*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

m688/a688 93.5% identity in 138 aa overlap

```

m688.pep      10      20      30      40      50      60
               VLHYPSSRFQAGKISVNKTLILALSALLGLAACSAERVSLFPSYKLKIIQGNLEPRVAAA
a688          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
               10      20      30      40      50      60
               VLHYPSSRFQAGKISVNKTLILALSALLGLAACSVERVSLFPSYKLKIIQGNLEPRAVAS

m688.pep      70      80      90      100     110     120
               LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
a688          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
               70      80      90      100     110     120
               LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKDRSNLT VYFENGVLVRTEG

m688.pep      130     140
               DVLQNAAEALKDRQNTDKPX
a688          ::::::::::: :||:|
               NALQNAAEALRVKQNADKQX
               130     140

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTCCAT CGATGCCCTAC CTGCCCCGCGA
101 TTCCCCGAAAT GCGCGAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTGTT CGGCACGCGG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGGCGTT GCCGCCATCG TATTGTCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTc ggtgcatgg tgcgcatTA TTATCCGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTG TGATGGTTGT GCCGCTGGCC
451 GCACCCATGG TCGGCGCATT GTTGCAGGGA TTGGGCGGAT GCGGGGCGAT
501 TTTCGTTTTC ttggcGgcgT ATTGCGCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTGTCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTC
601 GGGCTGGTGG CGGGCGCGTT CAAGCGCGTA TTGAAAACCC GTGCCCGGAT
651 GGGTtatCTG TTTTTTCAGG CATTACGCTT CGGTTTCGATG TTCGCCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCAGT TACGCCGCAC
751 CCGTACGCAT GGGTGTTCG ACTCAACATC ATCAGCATGA TGTTTTCAG
801 CCGCGTTACC GCGTGGCGGC TTAACAACCG CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTCGTC CAATTGCGG CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTTT TGCTGCGCG TCGCGTGCCT
951 GATGTTTTTC GTCGGTACGC AGGECCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGCGC GCAGCGCGAA CGCCGTGTCTG
1051 GGTGTATTCC GGTCTTAAT CGGCGCGGGC GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGAAGGAAA ACGAAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689 >:

g689.pep (partial)

```

1  ..SPPLPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFGTA FGQVAGGAVS DIKGRKEVAL TGLIVYCLAV AAVVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYSG RKAQMFALI GIILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPVLPG LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFQAFSFGSM FAFLTESFV YRQLYHVTPH
251 RYAWFSLNI ITMMFFSRVT AWRLKTGAHP QSILLRGIV QFAANPSQLA
301 AVLFFGLPPE WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTCCCGT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGCGG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCTGA AATGAGCGAA AAATGATGG CGGTTTTGAT
201 CGCGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCCG
351 CCGTTCCGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTTGT TTCGAGTGCC
451 GAACAGTCC TCAACCTGCG CGTCGTGCAG GCATTCCGTG CCGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGCT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCC TCCCAAGCCC GCCGTGCGCG GCAAAATCGG ACGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTCG ATGTTGCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACCAGC AGCTCTACCG TGTACGCCCT
901 CATCAATACG CTTGGGCGTT TGCACCAAC ATCATACGA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTG CCGCAACCT GTCCCACTC
1051 GCCCGCGTGC TGTTTTTTCG GTTGCCCGCG TTTTGGCTGC TGGTCGCTG
1101 CGTGATGTTT TCCGTCGCTA CGCAGGCGTT GGTGCGTGCA AACACGCAGG
1151 CGTGTGTTAT GTCCTATTC AAAGAAGAGG GCGGCAGCGC AAACGCGGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTCTCTGCAC GACGGTTTCG CAACCGTGAT GCGGCAACG ATGACCGCGT
1301 CCACCTCTTG CCGCATTCG CTTCTGTGGC TCTGCTGCA TCGTGGTGG

```

1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

m689.pep
 1 LLIHYIVPVR PVLPGLLLPP VCAGVLKFSV SAYCVFERRA VCLRIGREFM
 51 PSAHYPEMSE KIMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
 101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLIVYCLA VAAIVFVSSA
 151 EQLNLNRVVO AFGAGMTVVI VGAMVRDYS GRKAAQMFAL IGIIIMVVL
 201 VAPMVGALLQ GLGGWQAIIV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
 251 FGLVAGRFKR VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYRVTP
 301 HQYAWAFALN IITMMFFNRV TAWRLKTGVH PQSILLWGIV VQFAANLSQL
 351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
 401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
 451 KENGQSEYL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

	30	40	50	60	70	80
m689.pep	CAGVLKFSVSAYCVFERRAVCLRIGREFMPSAHYPEMSEKIMAVLMAMLVTLMPFSIDA					
g689	SPPLPPMSGKLMAVLMAVLVALMPFSIDA					
		10	20	30		
	90	100	110	120	130	140
m689.pep	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLA					
g689	LPAIPEMAQPLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLA					
	40	50	60	70	80	90
	150	160	170	180	190	200
m689.pep	AAIVFVSSAEQLNLNRVQAFGAGMTVVIVGAMVRDYSGRKAAQMFALIGIIIMVVLV					
g689	AAIVFASSTEQLLNLRAVQAFGAGMAVVIVGAMVRDYSGRKAAQMFALIGIIIMVPLA					
	100	110	120	130	140	150
	210	220	230	240	250	260
m689.pep	APMVGALLQGLGGWQAIIVFLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFKR					
g689	APMVGALLQGLGGWRAIFVFLAAYSPVLPGLVQYFLPNPFAVGGKIGRDVFGVLVAGRFKR					
	160	170	180	190	200	210
	270	280	290	300	310	320
m689.pep	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMMFFSRVT					
	220	230	240	250	260	270
	330	340	350	360	370	380
m689.pep	AWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMFSVGTQGLVGAN					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMFSVGTQGLVGAD					
	280	290	300	310	320	330
	390	400	410	420	430	440
m689.pep	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL					
	340	350	360	370	380	
	450	460				
m689.pep	LWLCSHRAWKENGQSEYLX					
g689	LWLCSHKAWKENEKKRIL					
	390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCGCT GTTGTGCGCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAACGTATGG CGGTTTTGAT
201 GGCATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCACG GCGTTCGGAC AGGTGGTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGCTCTA CTGCCTTGCC GTTGCCGCCA TCGTATTTGC TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCGGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCAGCA TTATTATCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCTT GCCAAGCCC GCCGTCGGCG GCAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCCG
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTCG ATGTTGCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCAAGTACG CTTGGGCGTT TGCATCAAC ATCATCACA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAC CGGCGTGCA CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTC GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGCAGG
1151 CGTGTTTTAT GTCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGCGCAC
1251 CTTCTTGAC GACGGTTCGG CAACCGTGAT GCGGCAACCC ATGACCGCGT
1301 CTACCTCTTG CGGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTCGCTGG
1351 AAAGAAACG GCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1  LLIHIVPVR PVLPGLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVQ AFGAGMTVVI VGAMVRDYS GRKAAQMFAL YGIIIMVVPL
201 VAPMVGALLQ GLGGWQALFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGREFR VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYHVP
301 HQYAWAFALN IITMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

```
m689/a689 99.1% identity in 459 aa overlap

      10      20      30      40      50      60
m689.pep  LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
          |||
a689      LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
          |||

      10      20      30      40      50      60
m689.pep  KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
          |||
a689      KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
          |||

      70      80      90      100     110     120
m689.pep  SDIKGRKPVALTGLIVYCLAVAAIVFSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS
          |||
a689      SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS
          |||

      130     140     150     160     170     180
m689.pep  GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQALFVFLAAYSLVLLGLVQYFLPKP
          |||
a689      GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQALFVFLAAYSLVLLGLVQYFLPKP
          |||
```

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```

|||||
a689      GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFRKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFGVLVAGRFRKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVT
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPP
          |||||
a689      HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMMAATFLH
          |||||
a689      FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMMAATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLWLCSHRAWKENGQSEYLY
          |||||
a689      DGSATVMAATMTASTSCGIALLWLCSHRAWKENGQSEYLY
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

```

g690.seq (partial)
1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCTCAAC CGATTGCAA
151 CCGGCCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCCTGC ACCCGCCGC CGGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACTGG AAACCGTTT CGGCTTACCC GCGCGCGGCT ATGACAACAT
351 ACAGCGGCTG CTgtttCCCG ACATCCGCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGcgcGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAAACCGC GgACAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCGGCAAC ATctgCCtaT
601 TTgaaccggc ACAACAacGG ACTTggcgGC AATTTCCAAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGA AACCAATCAC
701 TCTTCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCAGC CGTATTGTCG TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

```

g690.pep (partial)
1  MKNKTSSLPL WLAAIMLAAR SPSKEDKKE NGASAASSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQAIEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSOKTR GQGEPEKRRAR YFEVSATSAY
201 LNRHNNGLGG NFOYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDKPFLLD
251 IHFDENGKIT RIVVYEKNY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

```

m690.seq..
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
101 CCGTGTCTTC GTCCTCCGCG TCATCAGCTC CTTCCTCAAC CGATTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACTGG AAACCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCACGATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGGCG

```

1110

```

551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTTT ACGAAAATGG CAAAATCAGC CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
  1 MKNKTSLLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ
 51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEPEKTR YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPDKPFLLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690 89.3% identity in 408 aa overlap

      10      20      30      40      50      60
m690.pep MKNKTSLLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPSQTDLQPTASAPDNVK
          |||:||||:| |||:||||:| |||:||||:| |||:||||:| |||:||||:|
g690     MKNKTSLLPLWLAAIMLAARSPSKEDKTKEVGASAASSASSASSQTDLQPAASAPDNVK
          10      20      30      40      50      60

      70      80      90      100     110     120
m690.pep QAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
          |||:||||:| |||:||||:| |||:||||:| |||:||||:| |||:||||:|
g690     QAESAPLXNCTGLHPAAGIGDLIQQIAEHIDSDCLFALSHNELETRFGLPGGGYDNIQRL
          70      80      90      100     110     120

      130     140     150     160     170     180
m690.pep LFPDIRPEDPDYHQKITLAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
          |||:||||:| |||:||||:| |||:||||:| |||:||||:| |||:||||:|
g690     LFPDIRPEDPDYHQKIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
          130     140     150     160     170     180

      190     200     210     220     230     240
m690.pep GQGEPEKTRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
          |||:||||:| |||:||||:| |||:||||:| |||:||||:| |||:||||:|
g690     GQGEPEKTRARYFEVSATSAYLNRHNNGLGGNFQYIGQLPGYLMHGEMLENQSLFRLSNR
          190     200     210     220     230     240

      250     260     270     279
m690.pep ERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
          |||:||||:| |||:||||:| |||:||||:| |||:||||:| |||:||||:|
g690     ERNPDKPFLLDIHFDENGKITRIVVYEKNIY
          250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
  1 ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
 51 GACCGCGTGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTCT GTCCACGGCA TCCGCGCTT CGTCTTCCGC GCCCCAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCGG TCAAATTGCA CCGACCTGCA CCCCGCCACC GGCATTGACG
251 ATCTCATGCA GCAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTTCCCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAAG
451 CGCACGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGGCGA GGAGCCGAAA CGCACGCGTT ATTTTGAAGT TTCGGCAACC
601 CCTGCCTATT CGAGCCGCGA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

```

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701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTATAGACA TCCATTTTGA CGAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep
 1 MKNKTSLLL WLAAMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVFP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT
 201 PAYSSRHNNG LGGNFQYIGQ LPGAUKIHGE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
	MKNKTSLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPS---	QTDLPQTASAPD			
a690	MKNKTSLLLWLAAMLTACSPSKDDKTKEVGASAASTASASSAPQTDLPQTASAPD				
	10	20	30	40	50
m690.pep	60	70	80	90	100
	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI				
a690	NVKQAESVFPSPNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI				
	70	80	90	100	110
m690.pep	120	130	140	150	160
	QRLFPDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ				
a690	QRLFPDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ				
	130	140	150	160	170
m690.pep	180	190	200	210	220
	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGAUKIHGEMLNQSFLRL				
a690	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYIGQLPGAUKIHGEMLNQSFLRL				
	190	200	210	220	230
m690.pep	240	250	260	270	279
	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRX				
a690	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNLGRX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTCCTA CCGAACTGCG ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCCGCC CCTTCAAAAT
 201 GCGCGGCGAC AGGCGCGGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGGCGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACGCCAAC
 401 AGCAGCAAAT GTGGCTTCTT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGHNELRK IRAAFKMGD RARLKVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQGOHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691 97.2% identity in 144 aa overlap

      10      20      30      40      50      60
m691.pep VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFPNCDIRRLGLTQSOHNELRK
      |||||
g691      VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFPNCDIRRLGLTQGOHNELRK
      10      20      30      40      50      60

      70      80      90      100     110     120
m691.pep IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL
      |||||
g691      IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNREARDYVESRYHSSMDFAVDEL
      70      80      90      100     110     120

      130     140
m691.pep EIQRFFHILTPQQQMWLSSCLKX
      |||||
g691      EIQRFFHILTPQQQMWLSSCLKX
      130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQGOHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

```

      10      20      30      40      50      60
m691.pep VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDPQPNCDIRRLGLTQSQHNELRK
      |||
a691      VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPLNDFQPNCDIRRLGLTQSQHNELRK
      10      20      30      40      50      60

      70      80      90     100     110     120
m691.pep IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNARDYVESRYLSGMDFAVDEL
      |||
a691      IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNARDYVESRYLSGMDFAVDEL
      70      80      90     100     110     120

      130     140
m691.pep EIQHRFFHILTPQQQMWLSSCLKX
      |||
a691      EIQHRFFHILTPQQQMWLSSCLKX
      130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

```

g692.seq
1  GTATCGCACA CACGCTGTCG CTGTTCCGAA TCGATacGCC GGATTGCGCG
51  GAATGGCAGG GAATGGCGGA TTAAGGACA AAAATGCCGT CTGAACACGG
101 ATGCGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGT ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTGCGCGGT TTTgacGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGCTCT TGGAACAGGG CTTCGGTCAG CTTATGCCC GTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTGCGCGGC
401 AGTTGTGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCCCG
451 GATGTCGGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTTACAG ATCACCAGG CGCGTGCGAA GTTGGAcggG
551 TcgtTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGTTTGGCC GGATACAGTC CCAAAGGCGC GGTGCGCACT TGAAGGCTT
651 CGGTGATGTC CAGGTTGTGT TCTTTTTTGA AATCGTCAAG ATAGGGTTTG
701 TGTGCGAAGA CGTTGATGTC CAACTCGCCC TCCGCCAATG CCAGATTCCG
751 GCGCACATAG TCggTAAATT cgaccaatTT gacgGTGTAg cTTTTTTTCT
801 CCAGCTCGgc tTGGATTTGT TCTTTGACCA TATcgccgaa gtcgcccacg
851 gTCGTGCCGA agacgaTTTC TTTTTCGCGc GcgcCGTTAT CGGCAGAAGG
901 GCGGCGGgca gaggctgcGG GCGCGCTGTC TTTTtgaccG ccgCAGGCTG
951 CGAGGATGAG CGCGAGtgcg gcggcggaag ggGTTTGAA GAAGGTTTtC
1001 atATTTTCTc ctga

```

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

```

g692.pep
1  VSHTRCRCSE SIRRIWRNGR EWRIKGQKCR LNTDAVQTAS FYTTALEFGCA
51  FIPCGRVFVA LEAFVRVGFE RVGVIGLVYV FKPLAVFVGG FDGRPVDIGK
101 ARLLLEQGFQ LHAAYGVVA VDDGKIHVGA AARQLCGFKL DDFDVFQVFR
151 DVGFQCGQRI DAVFEFDPTQ FVQHHQGACE VGRVVRGRYG AAVFDFFQRF
201 QFARIQSQR GRHLEGFGDV QVVFVEIVK IGFVLEDVDV QLALRQCQIR
251 AHIVGKFQDF DGVAFFLQLG LDLEFDHIAE VAHGRAEDDF FFRAVIGRR
301 GGGRCGRAV FLTAAGCEDE RECGGKGFE EGFHIFS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

```

m692.seq
1  GTGTTGCACA CGCTTTGTCG CTGTTCCGAA TCGATACGCC GGATTGCGCG
51  GAATGGCAGG GAATGGCGGA TTAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTGCGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTCGGTCAG CTTATGCCC GTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGCG

```


1114

```

401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCCTCGGC
451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCGGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTGAGC ATCACCAGA CGCGGCGGAA GTTGGACGGG
551 TCGTTGGCGG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTGCGCACT TGGAAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGTCGCGC TTGGATTTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTGTG CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTGTCTTT TTGACCGCCG CAGCGGCGCA
951 GGATGAGCGC GAGTGGCGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

```

m692.pep
1 VLHTLCRCSE SIRRIIRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGFE RVGVIGLYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVFOVLG
151 DVRFQGGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVGRCYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVGGG
301 RSGCGGRAVF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

```

m692/g692 91.1% identity in 338 aa overlap

m692.pep      10      20      30      40      50      60
VLHTLCRCSESI RRIRNRNGREWRIKGQKCR LNTDTVQTASFYTTALFGCAFI PCGRGFVA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692          10      20      30      40      50      60
VSHTRCRCSESI RRIRNRNGREWRIKGQKCR LNTDAVQTASFYTTALFGCAFI PCGRVFVA

m692.pep      70      80      90      100     110     120
LEAFVRVGFERVGVIGLYVFKPLAVFVGGFDGRPV DIGKARFLEQGGFQLHAAAYGVVA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692          70      80      90      100     110     120
LEAFVRVGFERVGVIGLYVFKPLAVFVGGFDGRPV DIGKARLLEQGGFQLHAAAYGVVA

m692.pep      130     140     150     160     170     180
VDDGKIHVGAATRQLRGFKLDDFDVQVLGDVRFQGGQRI DAVFEFDPTQFVEHHQDAGE
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692          130     140     150     160     170     180
VDDGKIHVGAARQLCGFKLDDFDVQVFRDVGFGCGQRI DAVFEFDPTQFVQHHQGACE

m692.pep      190     200     210     220     230     240
VGRVVGRCYGAAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692          190     200     210     220     230     240
VGRVVGRCYGAAVDFDFQRFQFARIQSQRGRHLEGFQVQVFFFEIVKIGFVLEDVDV

m692.pep      250     260     270     280     290
QLALSQCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDFFFRRAVVG--
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692          250     260     270     280     290     300
QLALRQCQIRAHIVGKFDQFDGVAFFLQLGLDLFFDHIAE VANGRAEDDFFFRRAVIGRR

m692.pep      300     310     320     330
GGRSGCGGRAVFLTAAGGEDERECGGGKGFEFGFHIFSX
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692          300     310     320     330
GGGRGCG-RAVFLTAAGCEDERECGGGKGFEFGFHIFSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

```

a692.seq
1 GTGTTGCACA CGTTTGTCTG CTGTTCCGAA TCGATACGCC GGATTCGGCG

```

```

51 GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTCGGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGC CTTCAGCTC GACGATTTG ATGTTTTC A GGTTCGCGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCGGCACT TGGAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGCAAG ATAGGGTTT
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGTCGGG TTGGATTGT TCTTTGACCA TATCGCGGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTTCGCC GCGCCGTTGT CCGCGCGGCG
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACCGCGC CAGGCGCGCA
951 GGATGAGCGC GAGTGCAGCG GCGGAAAGGG TTTTGAAGAA GGTTCCTATA
1001 TTTTCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

```

a692.pep
1 VLHTLCRCSE SIRRIIRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFEV LEAFVRVGFE RVGVIGLGYV FKPLAVFVGG FDGRPDVIGK
101 ARFLEQGGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151 NVRFQCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVGGRGYG AAVFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

```

m692/a692 98.8% identity in 336 aa overlap

```

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRIIRNGR	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFEV
a692	VLHTLCRCSE	SIRRIIRNGR	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFEV
	10	20	30	40	50	60
	70	80	90	100	110	120
m692.pep	LEAFVRVGFE	RVGVIGLGYV	FKPLAVFVGG	FDGRPDVIGK	ARFLEQGGFQ	LHAAAYGVVA
a692	LEAFVRVGFE	RVGVIGLGYV	FKPLAVFVGG	FDGRPDVIGK	ARFLEQGGFQ	LHAAAYGVVA
	70	80	90	100	110	120
	130	140	150	160	170	180
m692.pep	VDDGKIHVGA	ATRQLRGFKL	DDFDVQVFG	CGQRI DAVFE	FDPTQ FVEHHQ	DAGE
a692	VDDGKIHVGA	ATRQLRGFKL	DDFDVQVFG	GNVRFQCGQ	RI DAVFE	FDPTQ FVEHHQ
	130	140	150	160	170	180
	190	200	210	220	230	240
m692.pep	VGRVVGGRGY	GA AVFDFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
a692	VGRVVGGRGY	GA AVFDFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
	190	200	210	220	230	240
	250	260	270	280	290	300
m692.pep	QLALSCQIR	AYIVGKLDQF	DGVAFFLQLG	LDLFFDHIAE	VADGRAEDDF	FFRAVVG
a692	QLALSCQIR	AYIVGKLDQF	DGVAFFLQLG	LDLFFDHIAE	VADGRAEDDF	FFRAVVG
	250	260	270	280	290	300
	310	320	330			
m692.pep	RSGCGGRAIF	LTAAGGEDER	ECGGKGFEF	GFHIFS		
a692	RSGCGGRAIF	LTAAGGEDER	ECGGKGFEF	GFHIFS		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

g694.seq
 1 TCGGCATTG TGTGCCCCA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
 51 AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
 101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
 151 TTCAATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
 201 CGGGCGCGGA CGCGCCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
 251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
 301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATGGGCG
 351 AACCGACCAC AATCAGATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
 401 GTTTGCCGGT TGGTCGTCGC ATAGCAGATG TCTTCCTTGT GCGGATTGCG
 451 GATATTGGGG AAACGCGCGT TCAGCGCGGC GATGATGTCT TTGGTTTCAT
 501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTC GGGGTTTCTG
 551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
 601 CGGTGCAAGC TGCCCCATCG TGCCTTCGAC CTCGGCGTGC CCCTTATGCC
 651 CGATCATGAT GATTTCACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
 701 TGCACTTTTC TCACCAGCGG GCAAGTCGCA TCAAATACCC GGAACCGCG
 751 CTCGCGCGCT TCCTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
 801 CCAGTGTCGC GCCCGGCGGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
 851 CCTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTGTGGA CGACTTCGTG
 901 GCGCACATAA ACCGGCGCGC CGAATTCTTC CAAAGCACGT TCGACAATAC
 951 TGATTGCCCC ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
 1001 ATGGTTTTCG CGTTCATAAG TTTTGCATTC CGTGTTTCTG CGGCATTAC
 1051 GTTTTTTTGC TNNATCTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
 1101 ACCGCACCGA CGCAGATAA

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

g694.pep (partial)
 1 SAFVLPKHPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPFAGH
 51 FMPPSAYGCQ YFPQHFRGR RACRYADFAF AFKPRALQVG RVVHHIRIDS
 101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
 151 DIGETRVRQG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
 201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHRFRQR ASRIKYPETA
 251 LRRFLHLRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQV V HDEFVDDFV
 301 AHINRRAEFF QSTFDNTDCP IHTGAEEARI GKDDGFSVHK FCIPCSGDIH
 351 VFLLXCLDGR YCQAPPTPHR RR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

m694.seq
 1 TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
 51 GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
 101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
 151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
 201 ATCCCGGTAT GGTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
 251 GCGCCTGCCG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
 301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
 351 CCACCTTCGC CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
 401 ATCAGCATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCCGGTT
 451 GGTGCTCGCA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
 501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
 551 TGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGTTT
 601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GGCACAAGCT
 651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG
 701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
 751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
 801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTCCGC
 851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
 901 CAGGTTGTCC ACGACGAATT TGTTGTGAAC GACTTCGTGG CGCACATAAA
 951 TCGGCGCGCC GAACCTCTCC AAAGCACGTT CGACAATACT GATT GCCCGA
 1001 TCCACACGAG CGCAGAAAGC GCGCGGATTG GCAAGGATGA TGGTTTCTC
 1051 GTTCATAAGC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCT
 1101 TGGGTTTAC GGTGGACGAT GTTGTTCAAC ACCGCCAACA CCGCACCGAC
 1151 GCAGATAA

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

m694.pep
 1 LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
 51 HNAFFRTLAF AYGFVPSPAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
 101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHALF CQLFDGGLPV

1117

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151 GRRADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPKR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNV DFVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

m694/g694 86.8% identity in 372 aa overlap

```

              10      20      30      40      50
m694.pep    LVSASGTRQKCR LKPVQTAFVLPKHS----TPASTFAQIGFGFALAAQLFGQDEHNAFFR
              :|||||  |||
g694         SAFVLPKHPALTPASTFAQIGFGFALAAQLLGQDEHDAFFR
              10      20      30      40

              60      70      80      90     100     110
m694.pep    TLAFAYGFVPPSAYGCQYFPHQHFGGRGRACRYADVFALKPCALQVACIIHHRIDSARC
              :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g694         APPFAHGFMPPSAYGCQYFPHQHFGGRGRACRYADFAFAFKPRALQVGRVVHHRIDSARC
              50      60      70      80      90     100

              120     130     140     150     160     170
m694.pep    RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRADIIFLVRIADIGETRVQRGDDV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g694         RHFAQAVAVGRIGRTDHNHDVALFRQLFDGGLPVGRRADVFLVRIADIGETRVQRGDDV
              110     120     130     140     150     160

              180     190     200     210     220     230
m694.pep    FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPKRSFDLDVPLMPDHDDFT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g694         FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARCKLPKRAFDLGVPLMPDHDDFT
              170     180     190     200     210     220

              240     250     260     270     280     290
m694.pep    VLGIQSGDFLMHFRHQASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g694         VLGIQSGDFLMHFRHQASRIKYPETALRRFLHRLRYAVCRINQCRARRHFRQVFNKHR
              230     240     250     260     270     280

              300     310     320     330     340     350
m694.pep    TFFTQVVHDEFVNVDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
              :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g694         AFFAQVVHDEFVNVDFVAHINRRAELFQSTFDNTDCPIHTGAEAAARIGKDDGFSVHKFCI
              290     300     310     320     330     340

              360     370     380
m694.pep    SFSDGINIFLLGFYGGRCCTPPTPHRRRX
              ||||:|  :  ||  :|||||
g694         PCSDGIHVFLXXLCDGRYQAPPTPHRRRX
              350     360     370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1  TTGGTTTCGG CATCCGGCAC ACGGCAAAAA TGCCGCTCTGA AGCCTGTTCAC
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCGGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCGGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCACGATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCTGTCGA TAGCAGATAT CTTCCTTGTT CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTCT GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GGCAGAGCT
651 GCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG

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1118

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701 ATTTACACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```

a694.pep
  1 LVASGTRQK CRLKPVQTAFLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
  51 HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHR IDSARCRHEA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
151 GRIADI FLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFQ VFNKHRTFFT
301 QVVHDEFVND FVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRRX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

m694.pep	10	20	30	40	50	60
a694	10	20	30	40	50	60
m694.pep	70	80	90	100	110	120
a694	70	80	90	100	110	120
m694.pep	130	140	150	160	170	180
a694	130	140	150	160	170	180
m694.pep	190	200	210	220	230	240
a694	190	200	210	220	230	240
m694.pep	250	260	270	280	290	300
a694	250	260	270	280	290	300
m694.pep	310	320	330	340	350	360
a694	310	320	330	340	350	360
m694.pep	370	380				
a694	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695. seq
1   TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTTGTGATC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGCTG
251 CCTCCTGTGC TTCCGTTTTC CCCGTTCCGG AGGCGAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGGACTATC TGGGAAGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTTGGAGCA TACGAAAATA
451 CACCCCTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACGGC
601 AGGTTTTCTG CCGCAGCCGC CTTGTTGAAG GGGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695. pep
1   LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCONSQRF QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPEGSRTM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRTYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQOKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695. seq
1   TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGGATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGCTCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGGAAGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCCTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCT
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CCGTTGAAA GGCAGCGGAC GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTC AATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695. pep
1   LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYKSG
201 KFSAASALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQOKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
g695	LPQTRPARRHHRQYFVERKGDARSGFCAACQNSQRFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
m695.pep	LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
g695	FDPASEKIMKTKLPLFIIWLSVSASCASVLPVEGSRTEMPTQENASDGIPYPVPTLQDR					
	70	80	90	100	110	120
m695.pep	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTGGGSASA					
g695	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDLDRKLKEHYLNTGGGSASA					
	130	140	150	160	170	180
m695.pep	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTGGGSASA					
g695	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDLDRKLKEHYLNTGGGSASA					
	130	140	150	160	170	180
m695.pep	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
g695	HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
	190	200	210	220	230	240
m695.pep	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
g695	HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
	190	200	210	220	230	240
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
	250	260	270	280	290	300
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
	250	260	270	280	290	300
m695.pep	AVRKRKX					
g695	AVRKRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

```

1  TTGCCTCAAG CTTGTCCGGC AAGCGGCAT CATTGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCAGC
101 GTCGGCATCC TCAAAGATTT TAATCAAAAC CTGCCGACG ATACGCCGAT
151 TGTCCCATCC ACCCTGCCCG TCGGCGACGG TTTGACCTG CTTCTGAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTTGGCTG TCCGTATCCG
251 CCGCCTGTTC TTCCCTGTT TCCGCAATA TTCAGGATAT GCGGCTCGAA
301 CCGCAGGCAG AGGCAGGTAG TTCGGACGCT ATTCCCTATC CCGTTCAC
351 TCTGCAAGAC CGTTTGATT ATCTGGAAG CACTCGTC CGCTGTGCA
401 ACGAAGTGA AACCTTAAAC GGCAAGTCA AAGCACTGA GCATGCGAAA
451 ACACACCTT CCAGCAGGCG ATACGTCAA AACTCGACG ACCGCAAGT
501 GAAAGAGCAT TACCTCAATA CCGAAGGCG CAGCGCATCC GCACATACCG
551 TCGAAACCGC ACAAACCTC TACAATCAG CACTCAAACA CTATAAAGC
601 GGCAGGTTT CTGCCGCTG CTCCTGTTG AAAGCGCGG ACGGAGGCGA
651 CGGCGGCAGC ATCGCGCAAC GCAGTATGTA CCTGTTGCTG CAAAGCAGGG
701 CGCGTATGGG CAACTGCGAA TCCGTCATCG AAATCGGAGG GCGTTACGCC
751 AACCGTTTCA AAGACAGCCC AACCGCGCCT GAAGCCATGT TCAAATCGG
801 CGAATGCCAA TACAGGCTT AGCAAAAAGA CATTGCAAGG GCGACTTGGC
851 GCAGCCTGAT ACAGACCTAT CCCGGCAGC CGGCGGCAA ACGCGCCGCC
901 GCAGCCGTGC GCAAACGATA G

```

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

```

1  LPOACPARRH HCHRQYFVER KGDARSGFRC AAQRRHPQRF *SKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSACSSPV SRNIQDMRL
101 PQAEAGSSDA IPYPVPTLQD RLDYLEGLTV RLSNEVETLN GKVKALEHAK
151 THPSSRAYVQ KLDLDRKLKEH YLNTGGGSAS AHTVETAQNL YNQALKHYKS
201 GRFSAAASLL KGADGGDGGG IAQRSMYLLL QSRARMGNCE SVIEIGGRYA
251 NREKDSPTAP EAMFKIGECQ YRLQKDIAR ATWRSLIQTY PGSPAAKRAA
301 AAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
a695	LPQACPARRHHRQYFVERKGDARSGFRCAAQRRHPQRFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
	70	80	90	100	110	
m695.pep	LDPASEKIMKIKLPLFIWLSVSASCASVSPVAGSQT---EMSTRENASDGIYPVPVPTL					
a695	FDPASEKIMKIKLPLFIWLSVSAACSS--PVSRNIQDMRLEPQAEAGSSDAIPYPVPVPTL					
	70	80	90	100	110	
	120	130	140	150	160	170
m695.pep	QDRLDYLEGRIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGS					
a695	QDRLDYLEGTLVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYLNTEGGS					
	120	130	140	150	160	170
	180	190	200	210	220	230
m695.pep	ASAHTVETAQNLNQALKHYKSGKFSAASLLKGADGGDGGGIAQRSMYLLQSRARMGN					
a695	ASAHTVETAQNLNQALKHYKSGRFSAAASLLKGADGGDGGGIAQRSMYLLQSRARMGN					
	180	190	200	210	220	230
	240	250	260	270	280	290
m695.pep	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRS LIQTYPGSPA AKR					
a695	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRS LIQTYPGSPA AKR					
	240	250	260	270	280	290
	300					
m695.pep	AAAAVRKRKX					
a695	AAAAVRKRKX					
	300					

The following partial DNA sequence was identified in *N. gonorrhoeae*
g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:
g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

m696.seq

```

1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGCTGCGCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGGCAGAA
251 GCCGCACTGT CTTAACATC GGACTCAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTTG GCTTCTTTCG AACAAAGCTG CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

m696.pep

```

1  LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LFFGLRTSC QGSRHHCNQ *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:
a696.seq

1122

```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTG GCTTCTTTCG AACAAAGCTG CAAGGCAGCC GCCATCATG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1   LGCRQAASHH FCQGNKLFEG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRLN
101 LLFGFLRTSC QGSRHHCNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696   100.0% identity in 120 aa overlap

          10      20      30      40      50      60
m696.pep   LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
          |||||
a696        LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
          10      20      30      40      50      60

          70      80      90      100     110     120
m696.pep   ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRLNLLFGFLRTSCQGSRHHCNQ
          |||||
a696        ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRLNLLFGFLRTSCQGSRHHCNQ
          70      80      90      100     110     120

m696.pep   X
           |
a696       X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCTA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCG
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 TGGCGTGTTT GTTGTACCG TAGGGGCGAA CTTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTA CTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCGGC GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCTCTCT TTCAGGCGGG CTGCTGTTT
551 CCGCATCGGC AGATGGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGTTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTGTGAAG TCGTGCCGGT AGCGGTGAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CACGCTGGG
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1   MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKGKGV
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

m700.seq

m700.pap

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGLFPWRIGKKGKGVSVGVSGSVGQLCVLLGFAFG					
g700	DMALTVLWLFVCTVGANLLALAVLGLSPWRIGGKKGKGVSVGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFMLSSLSGG					
g700	KLMCDIWMPSENAGMYCMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFI					
	190	200	210	220	230	240

1124

	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDA	AVGVGGAT	SMDFTLP	VIQAGGLE	VPVAVS	FGVVVNIAAPFLMVVFSALG
g700	LLMKRFPDA	AVGVGGAT	SMDFTLP	VIQAGGLE	VPVAVS	FGVVVNIAAPFLMVVFSALG
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTATATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG
151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGAC GATATGCGCT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AAACGTATGC GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTTC GTCAACCGCA GGGGTATTTCG
501 GTTGTCGGTC TGGTTTATGC TTTCATCTCT TTCAGCGGGG CTGCTGTTTG
551 CCGCATCCGGC AGACGGGTGT TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTTGGA CGAGAGCTGT
701 TCGCGCTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTC CGATGCGGCA
751 GTGGGGGTTC GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTCG
801 GGGTGCGGGC GGCTTGGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTTTC CGCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPFW RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 FFGWYSLSLG VMTEAYGAVW GSIALNLNLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMD FTLPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPFWRIKGKKGKGVSVGVSGSVGQLGCVLLGFAFG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLPFWRIKGKKGKGVSVGVSGSVGQLGCVLLGFAFG					
	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPFWRIKGKKGKGVSVGVSGSVGQLGCVLLGFAFG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLPFWRIKGKKGKGVSVGVSGSVGQLGCVLLGFAFG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

1125

	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
a700	LLFAASADGVSWVKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIALLLNDLARELFALAFIP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVIGAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
a700	LLMKRFPDAAVGVGGATSMDFTLPIRIGAGGLEAVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
a700	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

1	ATGTCCTGGC	ACATATTCCA	AGTTGCAGGG	ATACCGACCG	CTTCGATGGC
51	ACAATCTACG	CCGTCTTCGC	CGACGATGGC	GAAAACCTGT	TTGGAGACGT
101	CGCCGGAAGC	GGGGCTGATG	GTATGGGTCG	CGCCCAACTC	TTTCGCCGGT
151	TTCAAACGGT	TTTCGTCCAT	ATCGCACACG	ATAATGGCGG	CAGGGCTATA
201	CAGTTGGGCG	GTCACAAGG	CGGACATACC	GACAGGGCCG	GCACCTGCCA
251	TGAATACGGT	ATCGCCGGGT	TTACATCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTCG	GTAAAGCGTC	GCTCAACAGC	AGGGCGATTT	CTTCGTTGAC
351	GTTGTCGTGC	GGCGGCACGA	GGCTGTTGTC	GGCATAA	

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

1	MSWHIFQVAG	IPTASMAQST	PSSPTMAKTC	LETSPEAGLM	VWVAPNSFAG
51	FKRFSSISHT	IMAAGLYSWA	VNKADIPTGP	APAMNTVSPG	FTSPYCTPIS
101	WAVGKASLNS	RAISSLTLSG	GGTRLLSA*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

1	ATGTCCTGGC	ACATATTCCA	TGTAGCAGGG	ATACCGACGG	CTTCGATGGC
51	GCAATCCACG	CCGTCTTCGC	CGACGATGGC	AAAGACTTGT	TTGGATACTT
101	CGCCGGAAGC	AGGGTTAATG	GTATGGGTCG	CACCCAATTC	TTTCGCCAGT
151	TTCAAACGGT	TTTCGTCCAT	ATCGCAACAG	ATGATGGCGG	CGGGACTGTA
201	CAGTTGGGCG	GTCACAAGG	CGGACATACC	GACAGGGCCT	GCCCCAGCGA
251	TGAATACGGT	GTCGCCGGGT	TTGACATCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTCG	GCAAAGCGTC	GCTCAACAAC	AGGGCGATTT	CTTCGTTGAC
351	ATTATCGGGC	AGCGGAACGA	GGCTGTTGTC	GGCATAA	

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

1	MSWHIFHVAG	IPTASMAQST	PSSPTMAKTC	LDTSPEAGLM	VWVAPNSFAS
51	FKRFSSISQT	MMAAGLYSWA	VNRADIPTGP	APAMNTVSPG	LTSPYCTPIS
101	WAVGKASLNN	RAISSLTLSG	SGTRLLSA*		

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with menB

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTC	LDTSPEAGLMVWVAPNSFASFKRFSSISQT				
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTC	LETSPEAGLMVWVAPNSFAGFKRFSSISHT				

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	: : : : : :					
g701	IMAAGLYSWAVNKADIP TGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISLTLSC					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
	:
g701	GGTRLLSAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTTG CGCCCACTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCCA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTTC
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTLSG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQT					
	: : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASFKRFSISQT					
	10	20	30	40	50	60

	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	:					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
a701	SGTRLLSAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGtT ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGTGT TCGGCCGGC TCTGGCGAGG GATTCGTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTCCAGGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAAC TGCCCGGCGGT
351 CAGGATTTCG cggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

1127

```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51  CSQLVTVAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

m702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACTG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

m702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSQLVTVAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSQLVTVAP					
g702	MPCSKASWTS PGVATPGIRGMPLLRLPALARDSCPKGLMAKTAPASSTALSCSQLVTVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m702.pep	TMALGTSIAIRRMASRPTGVRVISRVGMPPSTRAWDKSM AVLKSSIAIT GTTAPAVKIS					
g702	MMALGISLAIRRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAIT GTTAPAVRIS					
	70	80	90	100	110	120
	130	140				
m702.pep	RGVSLDISVLRVEWGILLRWDRILX					
g702	RGVSK					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

a702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACTG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

a702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSQLVTVAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

1128

```

m702.pep  MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPA
|||||
a702      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPA
              10      20      30      40      50      60

              70      80      90      100     110     120
m702.pep  TMLGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMVLKSSIAITGTTAPAVKIS
|||||
a702      TMLGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMVLKSSIAITGTTAPAVKIS
              70      80      90      100     110     120

              130     140
m702.pep  RGVSLDISVLRVEWGILLRWDRX
|||||
a702      RGVSLDISVLRVEWGILLRWDRX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

```

g703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGCC GTTTACGACA ATATCAGCGG TTTTATATAA
451 GGCACGAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTGATGCCG
551 TTTTGAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCTT CTTTTCGACA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GCGGAACGG ATTGACCGTG CCGTctgTGc gcTGTgggt aaggCAACA
851 TCAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

```

g703.pap
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKDL E QGVPLYQAI KDLKKGEFTA TPLKNGDFYV VYYVNSREV
251 KVPSFDEMKG QIAGNLQAE R IDRVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

```

m703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAACA ATATTCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGCGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

```

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNDREV
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

```

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVVNTVVAAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVVNTVVAAQEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIKTQPVSEQEVKAAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	EAYALHIKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYYVNDREVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

```

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCTT CAAAACCGTT TGCGAGGCGG TAAATATG
351 CTTGAACGCG GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGTTT
401 CCGAGCAGGA AGTAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCTC AACGACCGTA CCAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGCGCA ATTTACGGCA ACGCCGCTGA

```


1130

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

```

a703.pep
  1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51  EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101  DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA AYDNISGFYK
151  GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201  VGYVPLKDL E QGVPPYQAI KDLKKGEFTA TPLKNGDFY VYYVNSDREV
251  KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

      10      20      30      40      50      60
m703.pep MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
a703      MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
      10      20      30      40      50      60

      70      80      90     100     110     120
m703.pep LENEVVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
a703      LENEVVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
      70      80      90     100     110     120

      130     140     150     160     170     180
m703.pep EAYALHIKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG
a703      EAYALHIKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG
      130     140     150     160     170     180

      190     200     210     220     230     240
m703.pep FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFY
a703      FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFY
      190     200     210     220     230     240

      250     260     270     280     289
m703.pep VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
a703      VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
      250     260     270     280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

```

a704.seq
  1  ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51  TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
101  GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
151  AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCCAAGAAAT
201  CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
251  TGGAAACCCA CGCGGGCACG CGCGAGGCGG TTTAATGCT CGGCGGCATC
301  ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TCGGTACAGA
351  CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
401  TCTGGGACGA CGGCAAAATC CGCCTTTCGG ACATTCTGTT GAAATCAGG
451  CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
501  CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
551  TGGGGATGAT GCAGACGATG ATGTTTCGCG TGCCGACCTA CCTTTACGGC
601  GGCGACATCG AACCCGATT CTGCAAATC CTCCATTGGG GCGGCTTTTT
651  AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
701  CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
751  GTCGCCATCA TCATGACCTT TATCGCCGGC GTTACAGCC TTGCGACAAA

```

```

801 TCGGGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCGCGCGAGA GGCTGGTGAA GCTGATTCCT GCGTTTTGCC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCCA GGCAGCTGTC GTCAAATTGA
1001 AGCGGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCGTTGAC
1051 GGCACGGTGC TGGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGGCGGC
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCGGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCTTGC GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GCGCGCGGAA GGTATTTTAA TCGCGGAAA GCAGGCAATC
1501 GAAACCTTCG CCCAAACCAC CGACATCATC TTCGACAAA CCGGCACGCT
1551 GACCCAAGGC AAACCGCGCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTCTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTTCA ACGGCAGCGT
1701 CCCCACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGGCGAACT GACCGTCAAC GCGGAAACAC AGGTTTGGG AGTTGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAA CAGAAGCGG
1851 CGGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCTGGGTGT CCGGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTTGGC
2151 GCAGGCAGAC GTATCCGCCG CCGCAGCGGG CGGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGCG AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAA GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAQS IIDAGLGSYY
51 KORTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIQ QLLRTDGI V RIDLNYSTHR CRVWDDGKI RLSIDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMQTM MFALPTYLYG
201 GDIEPDLQI LHWGGFLMVL PVVFYCAVPF YQGALRDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEAEQYAS SFIFGELLLA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTTDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSSQSGFQ AVFYLDPLK DSAAEAQRQL
651 AGKNLTLHIL SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEIDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVAQSIIDAGLGSYYKORTADAQKT
          |||
a704      MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVAQSIIDAGLGSYYKORTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIQQLLRTDGI
          |||
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIQQLLRTDGI

```

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	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNYSTHRCRVVDDGKIRLSDILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA					
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMMQTMFALPTYLYGGDIEPDLQILHWGGFLMVLPVVFYCAVPFYQGALRDLKN					
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGVYSLATNAGQGMYFESIAMLFFLLGGREFMEHIARRKAGD					
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLKAGDIVLVKPGETIPVDGTVLEGSSAV					
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRITGGGTRLSHIVRLLDRALAQKPR					
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAELEQYASSFIFGELLAVPVFIGWTLYADAHTALWITVALLVITCPCALSLATPTAL					
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGKQAIETLAQTTDII FDKTGTLTQGKPAVRRISLLRGTDEAFVLA					
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR					
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVAEISGKEPQTEGGGSAVYLGSGSGFQAVFYLTDPDKDSAAEAVRQLAGKNLTLHIL					
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAVAETARALGVAHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD					
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHI IRQNLWAGAYNIIAVPLA					
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMSFSSLA VLGNALRLHKGKMQSEKMPSEQX					
	790	800	810	820		

1	GTGTTCAATA	ATTTCcttgC	CTCTCTGCCG	TTTATGACGG	AAACACGGCG
51	TGATATGCTC	ATCAGCGCGT	TTGGGCCCAT	GGTTAAAGCC	GGCTTTACAG
101	TGTCCTTgCg	TTTGGGCATG	GCTTCTTTTC	TATATCGGAT	GATTATTGCC
151	GTAGCCGTTG	CTTTGGTAAG	AATCATGCCT	TCCGGCGGTA	TTTTCCAAAA
201	ATGCTTTTGT	AAGCTGGTGG	AATTTTATAT	TTCCGTCGTT	CGCGGTACGC
251	CGCTGTGTGT	TCAGCTTGTG	ATTGTGTTTT	ACGGCGTGCC	TGCGCTCGCG
301	ATCTATATCA	ATCCGATTCC	CGCCGCCATC	ATCGGCTTTT	CGCTCAATGT
351	CGCGCGCATC	CGTTCCGAAA	CCATATCGCG	GGCGATTTTG	TCCGTCGCCA
401	AAGGCGCAGT	GGAAAGCAGT	TTCTTCATCT	GATATGACTA	TATGCAGACG
451	TTCCGCCGCA	TCGTCGCACC	GCAGGCATTC	CGCGTCGCCG	TTCCGCCGTT
501	GAGCAACGAG	TGTTCCGGCT	TGTTCAAAAA	CACCTCGCTT	CGCCGCGTGG
551	TAAACGGTAAC	GGAGCTTTTC	CGTGTCCGAC	AGGAAACGGC	AAACCGCACT
601	TATGACTTTT	TGCCTGTCTA	TATCGAAGCT	GCATTGGTTT	ATTGGTGTTT
651	CTGTAAAGTG	CTGTTTTTTG	TTCAGGCGCG	TTTGGAAAAA	CGTTTCGACC
701	GTATTGTCGC	CAATAAA			

```

1 VENNFLASLF FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51 VAVALVRIMP SGGIFQKCLL KLVEFYISVV RGTELLVQLV IVFYGLPSVG
101 IYINPIPAAI IGFSNLVSGE ASETIRAAIL SAPKQWEAF FSIGMTYNQT
151 FRRIVAPQAF RAVVPLPNSE FIGLEKNTSL AAVKQVTEAG RVAQETANRT
201 YDELVPVYIEA ALVYWCFCVK LFLIQARLEK RFDRYVAK*

```

1	GTGTTCAAT	ATTTCCTTG	TTCGCTGCC	TTTATGACG	AAACACGCG
51	CGATATGAT	GTGACGCGT	TTTTCGCTAT	GGTCAAGGT	GGCTTCGCG
101	TCCTCTGCC	TTTGCCGCA	GCTTCTTTTC	TATACGGAT	GATGATTGCG
151	GTAGCCGTG	CTTTGGTGC	GATTATGCC	GCCGGCGCA	TCGTGCGGAA
201	AAATCCGCTG	AAATTTGGTG	AATTTTATAT	TTCCGCTATT	CGCGGTACGC
251	CGCTGTGTGT	TCAGCTGTGT	ATTGTGTTTT	ACGGGCTGCC	TTCCGTGCGC
301	ATCTATATCG	ACCCGATTCC	TGCCGCCATC	ATCGGCTTTT	CGCTCAATGT
351	CGCGGCATAC	GCTTCGGAAG	CCATACGCGC	GGCAATTTTG	TCCGTACCTA
401	AAGGCGCAAT	GGAAGCAGGT	TTCTCCATCG	GATGACCTA	TATGACAGC
451	TTCCGCCGCA	TTGTCGCGCC	GCAGGCATTC	CGCGTTGCCG	TGCCGCGCTT
501	GAGCAACGAG	TTTATCGGTT	TGTTTAAAAA	CAGCTCGCTC	CGCGGACGCT
551	TGACGGTAA	GGAAATTATC	CGCTGCGCGC	AGGAACGGC	AAACCGCATC
601	TATGACTTTT	TGCCCGTCTA	TATCGAAGCC	GCTTTGGTTT	ACTGGTGT
651	TGCTAAAGTG	CTGTTCTCTGA	TTCAGGCGCG	TTTGAAAAA	CGTTTCGACC
701	GCTACGTCCG	CAATAA			

```

1 VFNNFLASLF FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51 VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLQVL IVFYGLPSVG
101 IYIDPIPAAI IGFSNLVNGAY ASETIRTAAIL SVPKQVWEAF FSIGMTYMQT
151 FRIVAPQAF RVAVPPGSE FIFLGFRNTSL RFDRTQTELG RVAQETANRT
201 YDLFVPVYIEA ALVYWCFCVK LFLIQARLEK RFDRTVAY*

```

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```

      10      20      30      40      50      60
m705.pep  VFNNFLASLPFMTETRADMIVSAFLPMVKAGFVSLPLAASFVIGMMIAVAVALVRIMP
      10      20      30      40      50      60
g705      VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIAFVIGMIIAVALVRIMP
      70      80      90     100     110     120
m705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGVIYIDPIPAAIIGFSLNVGAY
      :||| :|

```

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```

g705      SGGIFQKCLLKLVEFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIAAIIGFSLNVGAY
           70          80          90          100         110         120

           130         140         150         160         170         180
m705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
g705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130         140         150         160         170         180

           190         200         210         220         230         239
m705.pep  AAVVTVTELFRAQETANRTYDFLPVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
           |||
g705      AAVVTVTELFRAQETANRTYDFLPVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
           190         200         210         220         230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA ATTTCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTGCGCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGTTT ACTGGTGT
651 TTGTAAAGTG CTGTTCTCTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIPAI IGFSNLVNGAY ASETIRAIL SVPKQWEAG FSGMTYMQT
151 FRRIVAPQAF RAVPPLSNE FIGLFKNTSL AAVVTVELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLIARLEK RFDYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

           10          20          30          40          50          60
a705.pep  VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           |||
m705      VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           10          20          30          40          50          60

           70          80          90          100         110         120
a705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAIIGFSLNVGAY
           |||
m705      AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAIIGFSLNVGAY
           70          80          90          100         110         120

           130         140         150         160         170         180
a705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
m705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130         140         150         160         170         180

           190         200         210         220         230         239
a705.pep  AAVVTVTELFRAQETANRTYDFLPVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
           |||
m705      AAVVTVTELFRAQETANRTYDFLPVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
           190         200         210         220         230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

```
g706.seq
1  ATGAACCTCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51  CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCCGgc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAtgaCCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCGcgatt tActccaacg cggtgGAacg taTGctcggg acggtcatcg
251 ggctgGGCGC GGGTTTGGgc gTTTATGGC TGAACCAGCA TTAttccac
301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggtacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCCCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCGC
501 CGCCAAATG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

```
g706.pep
1  MNSQRKRLS GRWLSYERY RHRLIHAVR LGGTVLFATA LARLLHLQHG
51  EWIGMTVFVV LGMLQFOGAI YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWLD SG
151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLAD C SKMIAEISNG
201 RRMTRERLEQ NMVKMRQINA RMVKSRSILA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTAAALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMREQ ISALVILLQR
351 TRRWLDAHE RQHLRQSLLE TREHG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

```
m706.seq
1  ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAAACGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

```
m706.pep
1  MNTSQRNRLV SRWLSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFOGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWLD SG
151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLAD C SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSILA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING
```

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQNRNLVSRWLSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	MNSSQRKRLSGRWLSYERYRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAIIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVTASALAGWAA					
g706	LGMLQFQGAIIYSNAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTIGTASALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
g706	VGKNGYVPMLAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMI AEISNGRRMTREERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
g706	FMLADNLADCSKMI AEISNGRRMTREERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTTELLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
g706	SMMEAMQHAHRKIVNTTELLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTAAALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALA EHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
g706	RHARRIRIDTAINPELEALA EHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLETREHGX					
g706	RQHLRQSLLETREHGX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

```

1  ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCTATGCTG GCGGGGCTGA
401 CGATGTGCAT GCTCATCGGC GACAACGGCA GCGAATGGTT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGCGGT TTCATGCTTG
551 CTGACAACCT GACCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGCGAACG CCTCGAAGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATTTG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCTT TATCAACGGC

```

1137

```

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
1  MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYKKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFD SG
151 LMRAMNVLIG AAIATAA AKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRS HLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

	10	20	30	40	50	60
a706.pep	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
m706	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a706.pep	LGMLQFQGA IYKKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
m706	LGMLQFQGA IYKKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a706.pep	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLIGAAIAIAAKLLPLKSTLMWR					
m706	VGKNGYVPM LAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a706.pep	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS HLAATSGESRISP					
m706	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS HLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a706.pep	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
a706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTRRKWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTRRKWLDAHE					
	310	320	330	340	350	360
	370					
a706.pep	RQHLRQSLLETREHSX					
m706	RQHLRQSLLETREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```

1  ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51  GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTT
201 TCTTCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGGCG AGTGTAAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTACAG
601 ATCAAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TCGGGGCGGC AAAACGACCG GCAAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGTT TTTATGTTTC ATATGGACGC
751 GGTGTGCGC ACAAAACGGA CTTGACTGAT GCCACCGGTA CGGAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGTGCCC GTAAAAAAT
851 GCGTGTTC TTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCGCGCGAG CGCATGCTTT GCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCCGC CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 CGCGGACCGG CATGCGCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGA
1251 CGCAGCCGCC CCATTTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAG TCAATGGAAC AAAACGCCGT TGGTTGCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTTCG
1551 CTTTCAGAGG GGCATATAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTT
1601 CGGCAAGCC GCTTCATAAA CCCAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1  MEIINDAELI RSMQRQQHID AELLTDANVR FEOPLEKNNY VLSEDETPCT
51  RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSA IIQPNMDSG ILKLRVSAGE IGDIREYKRR DGKSAEGSIS
151 AFNKKFFLYR NKILNLRDVE QGLENLRRLP SVKTDIQUIP SEEEKGSDLO
201 IKWQONKPIR FSGIDDAGG KTTGKYQGNV ALSFDNPLGL SDLFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNQ KOYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTMGRQ SMPAPEENG
401 DILPGTSRMK IITASLDAEA PFILGKQOFF YATAIQAWN KTPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYWQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1  NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51  GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCAATC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGCG
301 TTGGAAACCG TCGTCTGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NNTAAGCGAT TNGTTTTATG TTTCATATGG ACGCGGTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

```

```
751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCGTAT GAAATCATA ACCGCCGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTC AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTTCG CGGATTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TCAACTTGA
1451 ATTACAGTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```
a707.pep
  1 XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
 51 KLRVSAGEIG DIRYEKRDY KSAEGSISAF NKKXPLYRNL ILNLRDVEQG
101 LENLRLPSV KTDIPISE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDNGKQ YQSSLAERM
251 LWXXFXXTS VXMKLWTRQT KYIDDAEIE VQRRRSAGWE AELRHRLAYLX
301 RWQLDGKLSY KRGTMGRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
351 MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*
```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10      20      30
                                XKETAFTKGMCLGSNNLSRLQKAAQQILIVR
                                |||
m707      EDETPTCRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
              50      60      70      80      90      100

              40      50      60      70      80      90
a707.pep    GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNKKXPLYRNLKI
              |||
m707      GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDGKSAEGSISAFNKKFPLYRNLKI
              110     120     130     140     150     160

              100     110     120     130     140     150
a707.pep    LNLRDVEQGLNLRRLPSVKTDIPISEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
              |||
m707      LNLRDVEQGLNLRRLPSVKTDIPISEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
              170     180     190     200     210     220

              160     170     180     190     200     210
a707.pep    GKYQGNVALSXDNPGLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
              |||
m707      GKYQGNVALSFDNPLGLSDLFYVSYGRGLAHTDLTDATGTETESGSRYSVHYSVPVKK
              230     240     250     260     270     280

              220     230     240     250     260     270
a707.pep    WLFNFHNGHRYHEATEGYSVNYDNGKQYQSSLAERMLWXXFXXTSVXMKLWTRQTY
              |||
m707      WLFNFHNGHRYHEATEGYSVNYDNGKQYQSSLAERMLWRNRLHKTSVGMKLWTRQTY
              290     300     310     320     330     340

              280     290     300     310     320     330
a707.pep    KYIDDAEIEVQRRRSAGWEAELRHRLAYLXRWQLDGKLSYKRGTMGRQSMPEENGGGTI
              |||
m707      KYIDDAEIEVQRRRSAGWEAELRHRLAYLNRWQLDGKLSYKRGTMGRQSMPEENGGDIL
              350     360     370     380     390     400
```

1140

```

          340      350      360      370      380      390
a707.pep  PXXSRMKIITAGLDAAAPXMLGKQFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG
          | : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
m707      PGTSRMKIITASLDAAAPFILGKQFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG
          410      420      430      440      450      460

          400      410      420      430      440      450
a707.pep  EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
m707      EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
          470      480      490      500      510      520

          460      470      480
a707.pep  VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
m707      VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          530      540      550      560

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

```

g708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAA
301 CCCGACAGTG CCGAAATCAA CAACAAC TAC GGTGGTTC TGTGCGGCAG
351 GCTCAACCGC CTGCGCAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAATGCT GCGCGGCAG TTGGCGGATG CCGATTACTA CTTTAAAAAA
601 TACCAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAATTTGCC AAAGCCCTCG GCAACGTGCA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAATTTT CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

```

g708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLKVNDAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFLA EAYLKRS LAA QPQFPAPFKE LARTEMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNVQRAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

```

m708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAA
301 CCCGACAGTG CCGAAATCAA CAACAAC TAC GGTGGTTC TATGCGGCAG
351 GCTCAACCGC CTGCGCAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAATGCT GCGCGGCAG TTGGCGGATG CCGATTACTA CTTTAAAAAA
601 TACCAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAATTTGCC AAAGCCCTCG GCAACGCACA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAATTTT CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.pep

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKQ ESFRQALSIE
101 PDSAEINNNY GWFLCGRNLN PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLAA QPQFPFPAKE LARTKMLAGQ LGDADYYFFK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

m708/g708 99.2% identity in 253 aa overlap

      10      20      30      40      50      60
m708.pep MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
|||||
g708      MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
      10      20      30      40      50      60

      70      80      90     100     110     120
m708.pep DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRNLN
|||||
g708      DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRNLN
      70      80      90     100     110     120

      130     140     150     160     170     180
m708.pep PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFPFPAKE
|||||
g708      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFPFPAKE
      130     140     150     160     170     180

      190     200     210     220     230     240
m708.pep LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF
|||||
g708      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNVQAAYEYEAQLQANF
      190     200     210     220     230     240

      250
m708.pep PYSEELQTVLTGQX
|||||
g708      PYSEELQTVLTGQX
      250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTCGCTGGC TGGTCCGTGC CGAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCGACAGTG CCGAAATCAA CAACAAC TAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CTGCGCAAT CTATGGCATA TTTGACAAA GCCCTGGCCG
401 ACCCCACNTA CCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGCGGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRNLN PAESMAYFDK ALADPTYXP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLAA QPQFPFPAKE LARTKMLAGQ LGDADYYFFK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLAGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLAGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIIYQYLVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRLNR					
m708	DALKSDPKNELAWLVRAEIIYQYLVNDKAQESFRQALSIPKPSAEINNXYWFLCGRLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT  TCAATCCTT  ACTCGATATG  CCGCGCGGTG  AGGCACTTGC
51  CGTCGTCGTC  GCTCTGATTG  CCGCAATGGG  CTATACCATC  ATTTCAATTG
101 AGTGGCTGCC  GCATATGTCC  ATTATTGCCG  CCATCGTCGT  GCTGATTTTG
151 TACGGCTTGG  CGCGCGGTTT  GAAATACAAC  GATATGCAGG  CAGGGATGAT
201 AGGCGCGTTG  AATCAGGGTA  TGGGCGCGGT  TTACCTGTTT  TTCTTCATCG
251 GGTGATGGT  CAGCGCGCTG  ATGATGAGCG  GCGCGATTCC  GACGCTGATG
301 TATTACGGTT  TCGGGCTGAT  TTCCCGGACT  TATTTTATT  TTTCCGCCTT
351 CGCGCTGTGT  TCCGTATCG  GCGTGTCCAT  CGGCAGCAGC  CTGACCGCCT
401 CGCCACTGT  CGCGGTTGCC  TTTATGGGGA  TGGCGCGCGC  GTTTCAGGCC
451 GATATGGCGA  TGACGgcggg  cgcgattgTT  tccggTGTGT  TTTTCGGCGA
501 TAAATGTCC  CCGCTTCCG  ACACCACGGG  CATTTCGCG  TCCATCGTCG
551 GTATCGACCT  GTTTGAACAC  ATCAAAAACA  TGATGTACAC  CACCATCCCT
601 GCGTGGCTTA  TCAGCGCGGC  ACTGATGCTT  TGGCTTCTTC  CCAGCGTCGC
651 CGCGCAGGAT  TTGAACAGCG  TCGAATCCTT  CCGCAGCCAG  CTTGAAGCCA
701 CGGGATTGGT  GCACGGCTAT  TCGCTGATTC  CGTTTGCACT  GTTGTGCTGT
751 TTGGCATTGA  TGCGCGTCAA  TGCCGTGGTC  GCCATGCTCT  TTACCGTCAT
801 TGCCGCCGTT  GCCGTAACGT  ATCTGCACAG  CACGCCCGAT  CTGCGTCAGC
851 TCGCGCGGTG  GTTTTATGGC  GGCTACAAAC  TCGAAGGCGA  AGCGTTTAAA
901 GACATTGCCA  AACTGATTTC  GCGCGGCGGC  TTGGAGAGTA  TGTCTTTTAC
951 GCAGACCATC  GTTATCCTCG  GTATGAGTTT  GGGCGGGCTG  CTGTTTGC GC
1001 TCGGTGTGAT  TCCTTCCTTG  CTGGAGGCCG  TCCGTACCTT  CTTGACGAAT
1051 GCCGGACGCG  CGACGTTTCA  CGTTGCCATG  ACTTCGGTCG  GGGTCAATTT
1101 CCTGATTGGA  GAGCAATATT  TGAGCATCCT  GCTTCGGGA  GAAACGTTCA
1151 AATCCGTTTA  CGACAACTC  GGCCTGCATT  CGTGCAACCT  GTCGCGGACT
1201 CTGGAAGATG  CGGGGACGGT  GATTAACCCG  CTCGTGCCGT  GGAGCGTGTG
1251 CGGCGTATTT  ATCAGCCACG  CCCTTGGCGT  ACCCGTTTGG  GAATATCTGC
1301 CTTATGCCTT  TTTCTGTAT  TTGAGTTTGG  CTTTAACCTT  GTTATTCGGC
1351 TGGACGGGGC  TGACTTTGAG  CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDM  PRGEALAVVV  ALIAAMGYTI  ISLEWLPHMS  IIAAIVVLIL
51  YGLARGLKYN  DMQAGMIGAL  NQMGAVYLF  FFIGLMVSAL  MMSGAIPTLM
101 YYGFGLISPT  YFYFSAFALC  SVIGVSISS  LTACATVGA  FMGMAAFQA
151 DMAMTAGAIV  SGVFFGDKMS  PLSDTTGISA  SIVGIDLEH  IKNMYYTTP
201 AWLISAALML  WLLPSVAAOD  LNSVESFRSQ  LEATGLVHGY  SLIPFALLVV
251 LALMRVNAV  AMLETVIAAV  AVTYLHSTPD  LRQLGAWFYG  GYKLEGEAFK
301 DIAKLISRG  LESMFFTQTI  VILGMSLGL  LFLAGVIPSL  LEAVRTFLTN

```

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETEKPVYDKL GLHSCNLSRT
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTLSKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTTG AGGCACTTGC
51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTGG
101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGCGCGGAT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTTCTCCTT
351 CCGCGTGTGT TCCGTATCG GCGTGTCCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGCGGCG GTTTCAGGCC
451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGGCGCAT TTTTGGCGA
501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG
551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
601 CGGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTGCG
651 CCGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTG CGTTTGCCTT GTTGGTCATT
751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
801 GGTTCGCCGT GCTGTAACGT ATCTGCACAG CACGCGCGAT CTGCGTCAGC
851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGCGCA AGCGTTTAAA
901 GATGTTGTCA AACTGATTTT CCGCGCGGCT TTGGAAGTA TGTTTTTCAC
951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGCCT
1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
1051 GCCGGACGCG CGACGTCAG CGTTGCCATG ACTTCGCTCG GGGTTAATTT
1101 CCGATCGGCG GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTCA
1151 AATCCGTTTA CGATAAGCTC GGTCTGCATT CCGCAATCT GTCCGGGACG
1201 CTGGAAGATG CCGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
1251 CCGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCTT GTTATTCGGT
1351 TGGACGGGCG TGACTTTGAG CAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAIVVLIL
51 YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGGLISPT YFYFSSFALC SVIGVSIGSS LTTTCATVGA FMGMAAFQA
151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFEH IKNNMYTTIP
201 AWLISAALML WLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGANFYG GYKLEGEAFK
301 DVVKLISRGG LESMFFTQTI VILGMSLGLL LFALGVIPSL LEAIRFTLTN
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETEKPVYDKL GLHSRNLST
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTLSKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVV	ALIAAMGYTIISLEWLPHMS	IIAIVVLILYGLARGLKYN			
g709	MFAFKSLDDMPRGEALAVVV	ALIAAMGYTIISLEWLPHMS	IIAIVVLILYGLARGLKYN			
	10	20	30	40	50	60
	70	80	90	100	110	120
m709.pep	DMQQGMIGALNQGMGAIYLF	FFIGLMVSALMMSGAIPTLM	YYGFGGLISPTYFYFSSFALC			
g709	DMQAGMIGALNQGMGAVYLF	FFIGLMVSALMMSGAIPTLM	YYGFGGLISPTYFYFSAFALC			
	70	80	90	100	110	120
	130	140	150	160	170	180
m709.pep	SVIGVSIGSSLTTCATVGVA	FMGMAAFQADAMTAGAIV	SGAFFGDKMSPLSDTTGISA			
g709	SVIGVSIGSSLTACATVGVA	FMGMAAFQADAMTAGAIV	SGVFFGDKMSPLSDTTGISA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m709.pep	SIVGIDLFEHIKNNMYTTIP	AWLISAALMLWLLPNVAAQD	LNSVESFRSQLEATGLVHGY			
g709	SIVGIDLFEHIKNNMYTTIP	AWLISAALMLWLLPSVAAQD	LNSVESFRSQLEATGLVHGY			
	190	200	210	220	230	240

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLF	TMVMVAVV	TYLHSTPDLRQLGAWFYGGYKLEGEAFK			
g709	SLIPFALLVVLALMRVNAVVAMLF	TVIAAVV	TYLHSTPDLRQLGAWFYGGYKLEGEAFK			
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMFFFTQ	TIVILGMSLGLL	FALGVIPSLLEAIR	TFLT	NAGRATFS	VAM
g709	DIAKLISRGGLESMFFFTQ	TIVILGMSLGLL	FALGVIPSLLEAVR	TFLT	NAGRATFS	VAM
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQYLSILLS	GSETFKPVYDKLGLHSRNL	SRTLEDAGT	VINPLVPWSV	CGVGF	
g709	TSVGVNFLIGEQYLSILLS	GSETFKPVYDKLGLHSCNLS	SRTLEDAGT	VINPLVPWSV	CGVGF	
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFC	YLSALTL	LF	GTGLT	LSKKX	
g709	ISHALGVPVWEYLPYAFFC	YLSALTL	LF	GTGLT	LSKKX	
	430	440	450	460		

a709.seq

a709.pcp

1	MFAFXSLDDM	PRGEALAVVV	ALIAAMGYTI	IXLEWLPHMS	IIAAIVLVLI
51	YGLARGLKYN	DMQQQMIGAL	NQVGMAIYLF	FFGLTMVSLA	MMSGXAIPTLA
101	YYGFGLSIPT	YFYFSAFALC	SVIGVSIGSS	LTTCATVGVA	XMGXXXAFXA
151	XXGXXXXXIV	XXAXGXKMS	PLSDTXGXA	SVIGIDLFEB	IKNMYYTITP
201	AWLISXKLML	XLLPSVAAQD	LNSVESFRSQ	LEATGLVHCY	SLIPFALLVV
251	LALMRNVAUV	AMLFVTIAAV	AVTYLHSTPD	LRQLGAWPYG	GKLEGEAXX
301	DIAKLISRGG	LESMTFTQTI	VILGMSLGLL	LFALGAIPSL	LDVARSFLTN
351	AGRXTFSVAM	TSVGNVFLIG	EQYLSILLSG	ETFKPVYDKL	GLHSRNLST

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTSLKK*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTIIIXLEWLPHMSIIAAIVVLILYGLARGLKYN					
m709						
	10	20	30	40	50	60
a709.pep	DMQQGMIGALNQGMGAIYLLFFFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSAFALC					
m709						
	70	80	90	100	110	120
a709.pep	DMQQGMIGALNQGMGAIYLLFFFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSAFALC					
m709						
	70	80	90	100	110	120
a709.pep	SVIGVSIGSSLTTCATVGVAXMGXXXAFXAXMXXXXXXIVXXAXXGXKMSPLSDTXGXSA					
m709						
	130	140	150	160	170	180
a709.pep	SVIGVSIGSSLTTCATVGVAXMGXXXAFXAXMXXXXXXIVXXAXXGXKMSPLSDTXGXSA					
m709						
	130	140	150	160	170	180
a709.pep	SIVGIDLFEHIKNMYYTTIPAWLISXXLMLXLLPSVAAQDLNSVESFRSQLEATGLVHCY					
m709						
	190	200	210	220	230	240
a709.pep	SIVGIDLFEHIKNMYYTTIPAWLISXXLMLXLLPSVAAQDLNSVESFRSQLEATGLVHCY					
m709						
	190	200	210	220	230	240
a709.pep	SLIPFALLVVLALMRVNAVAMLFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAXX					
m709						
	250	260	270	280	290	300
a709.pep	SLIPFALLVVLALMRVNAVAMLFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAXX					
m709						
	250	260	270	280	290	300
a709.pep	DIAKLISRGGLESMFFTQTIVILGMSLGGLLFALGAIPSLDAVRSFLTNAAGRXTFSVAM					
m709						
	310	320	330	340	350	360
a709.pep	DIAKLISRGGLESMFFTQTIVILGMSLGGLLFALGAIPSLDAVRSFLTNAAGRXTFSVAM					
m709						
	310	320	330	340	350	360
a709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
m709						
	370	380	390	400	410	420
a709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
m709						
	370	380	390	400	410	420
a709.pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
m709						
	430	440	450	460		
a709.pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
m709						
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAACCC	ACGAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGGCGGAAA	AGCTGGCGAT	GTCCGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCCGCGTTT	GGAGCAGTTG
151	GCTCAGATT	TCAAAATCGA	TATGTGGGAC	TTGCTCAAAT	CGGGCGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGGC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTT	AAAAATGGAG

m710.pep

1	METHEKIRLM	RELNKSQED	MAEKLAWSAG	GYAKIERGET	QLNIPRLRQL
51	AQIFKIDMWD	LLKSGGGGMV	FQINEGDSGG	DIALYASGDV	SMKIEFLKME
101	LKHCKEMLEQ	KDKEIELLRK	LTETV*		

```
a710.seq
  1  ATGGAACCC  ACGAAAAAAT  CCGCTGATG  CGGAATTGA  ATAAATGGTC
51  CCAGGAGGAT  ATGGCGGAA  AGCTGGCGAT  GTCCGCAGCG  GGGTATGCCA
101 AAATCGAAGC  AGCGAAACG  CAGTTGAAT  TCCCGCGTTT  GGAGCAGTTT
151 CGCGAGATTT  TCAAATTGA  TAGTGGGAC  TTGCTCAAT  CGGCGCGCGG
201 CGGGATGGTG  TTGCAGATTA  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251 CAATCTATAC  CGCTCAGGAT  GCATCNGGTA  AAGCTGGATT  TGTAAATATG
301 GAATTAACAC  ACTGTAAGA  AATGTTGGAA  CACAAAGACA  AAGAAATCGA
351 GCTGCTCCGC  AAGCTGACCG  AAACCGTTTA  A
```

```
a710.pep
1  METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
51  AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
101 ELKHCKEMLE HKDKETLLR KLTETV*
```

[illegible]

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a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

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1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```

m711.seq
1  ATGCCCCGCGC CTGATTGTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCTATAAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATT TAAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCCTATAAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGT TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```

m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLASEIA KVYTIARMTD
51  LDMNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
151 SRTTPAHSAL DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFSTS FKQLEKEFYE VKQRLDIDKG
301 PKPEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```

a711.seq
1  ATGCCCCGCGC CTGATTGTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCTATAAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATT TAAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG

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1148

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901 CCGGATAAAG AGCAGAAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```

1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFDYNAGRM
251 NYRPDLKDYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	10	20	30	40	50	60
	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEYVKQRLDIDGK					
m711	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEYVKQRLDIDGK					
	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

1149

a711.pep

AKFMAKKKVLKX

|||||

m711

AKFMAKKKVLKX

430

1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```

m712.seq
1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TCCCGTACAA GGTTTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCCGA CAAGGCTCGC TGGCGCATTG ATGGTTCGCG CAAGCATTGT
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTCCCGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GGCGGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTTCA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGGTGTTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGCGA CTAATCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GGCGCGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCCGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTGA
1401 TTTGATTTTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```

m712.pep
1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKVL MVAFMLTAGI
51  QPALEPVQLF SDAEAADLFG QGSLAHLNVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAYL
301 AFEEDPAKPL NTLKIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSAANTDDPA LLDITTTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451 IPADVNLH VFAGRIDLIL *

```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```

m713.seq
1   ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCCTTTG GGCAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
651 TTTTGTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGGTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```

m713.pep
1   MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSORHKG SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMIDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLLKVVYKD PTMTLHRPKT
251 VVVSADANLA ALQQAQKQL ADWRLEGFTL TITVGGHKTR DGVLWQPLR
301 VHVIDDEHGI DAVFFLMGRR FMLSRLMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKKGKG GKQAETAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```

a713.seq
1   ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
651 TTTTGTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGGTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG

```

1152

1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDV VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTFLL QSHGRSGDSA KHDWKVYKD PTMTLHRPKT
251 VVSDADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGGKG GKKQAETAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDVIGRLGPEAAIPDLSGESCE					
m713	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDVIGRLGPEAAIPDLSGESCE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
m713	VVIDGQIVMTGIIGSQRHGKSKGRELSSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a713.pep	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGVD					
m713	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a713.pep	YSSPPVATLCWSRTDSRRNIERMDIEWDTDNRFSEVTFLLAQSHGRSGDSAKHDLKVYKD					
m713	YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVTFLLAQSHGRSGDSAKHDLKVYKD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a713.pep	PTMTLHRPKTVVSDADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGQR					
m713	PTMTLHRPKTVVSDADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGLR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a713.pep	VHVIDDEHGIDAVFFLMGRRFMSRMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
m713	VHVIDDEHGIDAVFFLMGRRFMSRMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
	310	320	330	340	350	360
	370	380				
a713.pep	KGVSHKGGKGGKKQAETAVFEX					
m713	KGVSHKGGKGGKKQAETAVFEX					
	370	380				

1153

g714.seq not found yet

g714.pap not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```

m714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
 51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101  TGGATGCGGT GGCAGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151  CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201  CGGTACGGGC AAAAACCGCC AGCACCCTGT GTTGCCCGTC ATGGCCAAGC
251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351  TGTAAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401  GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATCCGCGGCC
451  GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551  CCTACCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```

m714.pap
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
 51  RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```

a714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
 51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101  TGGATGCGGT GGCAGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151  AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201  CCGTACGGGC AAAAACCGCC AGCGCCGTGT GTTGCCCGTC ATGGCCAAGC
251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351  TGTAAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401  GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATCCGCGGCC
451  GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551  CCTACCGATA A

```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```

a714.pap
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
 51  SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

a714/m714 98.9% identity in 186 aa overlap

```

      10      20      30      40      50      60
a714.pap MSYQDILRGLLPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW
          |||
m714      MSYQDILRGLLPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPRSAGQMLADW
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
a714.pap ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR
          |||
m714      ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
a714.pap AGDRLAPQEI MWVWHVNVRG GNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
          |||

```


1154

m714 AGDRLAPQEIMVWHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTG
 201 GGGTCGCTCG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTG
 201 GGGTCGCTCG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
 51 GGCGCCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

1155

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq
 1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHNSAHG SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGA-----				
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGASKSAEGSCGASKSAEG				
	10	20	30	40	50
					60
	60	70	80	90	100
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX				
g716	SCGAASKAGEGKCGEGKCGATVKKAKHHTKASKAKAKSAEGKCGEGKCGSKX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq
 1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHNSAHG SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC

1156

```

51  GGGTTTtagcc  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCCCTG  CGGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCGCCGCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCCCG
601  CCGCGCCGCT  TTTGCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATT  CGTTCGGCGG  GCGGCGATTA  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAAATCCG  CCGCCGCCCT  GCTTGCCCTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCTCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGccgc
1001  cgctGTTTT  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGGTTGCCTG  TGCCGCCTCA  TTCTGGTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCTGCCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTT  TGCCTgCCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCcctgttt  gccggtgtAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AAATTGACAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

```

g717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCIGLDQA YVREYAAAD KDTLFKTLFL PPLLFSAAIA ALLLSRPSLP
101  SEILFSLDDA AAGIGLVLE FSFLPIRFL LVLRMGRAL AFSSAQLVPK
151  LAILLLLPLT VGLLHFPANT SVLTAVYALA NLAAAFLLF QNRCRLKAVR
201  RAPFSPAVLH RGLRYGIPLA LSSLAYWGLA SADRLFLKRY AGLEQLGVYS
251  MGISFGGAAL LLOSIFSTVW TPYIFRAIEE NATPARLSAT AESAALLAS
301  ALCLTGIFSP LASLLLPENY AAVRFTVVSC MLPLPFYTLT EISGIGLNVV
351  RKTRPIALAT LGALAAANLL LGLAVPSSGT RGAAVACAAS FWLFFVFKTE
401  SSCRLWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAAAYLAG
451  CILRHRKNLH KLFHYLKKQG FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

```

m717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGGTTTtagcc  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCccccCGG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGCGGG  GCTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTTCAAAAC  CCTGTTCCCTG  CGGCCGCTGC
251  TGTTGCGCGC  CGCGATAGCC  GCCCTGCTGC  TTTCGCCGCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCCCG
601  CACGACCCGT  TTTGCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATT  CGTTCGGCGG  GCGGCGATTA  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAAATCCG  CCGCCGCCCT  GCTTGCCCTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCTCTCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTT  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTTGCCTG  TGCCGCCTCA  TTCTGGCTGT  TTTTGTGCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTT  TGCCTGACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCTGTTT  GCCGGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AGATTGACAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep
 1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
 51 SVLCLGLDQA YVREYYATAD KDTLFTKTLF PLLSAAAIA ALLSRPSLP
 101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVPK
 151 LAIIILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
 201 HAPFSPAVLH RGLRYGPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
 251 MGISFGGAAL LFQSIESTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
 301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
 351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
 401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAAYLAG
 451 CILRHRKDLH KLFHYLKKQG FPL*

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
g717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
m717.pep	70	80	90	100	110	120
	YVREYYATADKDTLFTKTLFPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
g717	YVREYYAADKDTLFTKTLFPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
	70	80	90	100	110	120
m717.pep	130	140	150	160	170	180
	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAIIILLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAIIILLPLTVGLLHFPANTSVLTAVYALA					
	130	140	150	160	170	180
m717.pep	190	200	210	220	230	240
	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGPIALSSIAWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGPIALSSIAWGLASADRLFLKKY					
	190	200	210	220	230	240
m717.pep	250	260	270	280	290	300
	AGLEQLGVYSMGISFGGAALLFQSIESTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSIESTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
	250	260	270	280	290	300
m717.pep	310	320	330	340	350	360
	ALCLTGIFSPLASLLPENYAAVRFIVVSCMLPPLFCTLAIEISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPLASLLPENYAAVRFIVVSCMLPPLFCTLAIEISGIGLNVVRKTRPIALAT					
	310	320	330	340	350	360
m717.pep	370	380	390	400	410	420
	LGALANLLLGLAVPSGGARGAAGVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALANLLLGLAVPSGGTRGAAGVACAASFWLFFAFKTESSCRLWQPLKRLPLYMHTLF					
	370	380	390	400	410	420
m717.pep	430	440	450	460	470	
	CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					
g717	CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					
	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
 51 GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
 101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
 151 TCGGTGTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
 201 CGCCGCCGAC AAAGACACTT TGTTCAAAAC CCTGTTCTTG CCGCCGCTGC

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTC
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCCGTGACG GTCGGGCTGC TGCACTTTCC
501 GGCGAACACC GCCGTCCTGA CCGCGCTTTA CGCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCCGTCCGG
601 CGCGCACCGT TTTTCATCCG CGTCCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCGCG
851 CCGCCCGCCT CTCGGCAACG GCAGAAATCCG CCGCCGCCCT GCTTGCCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCCTCCC TCCTGCTGCC
951 GGAAAACTAC GCCGCCGTCC GGTTTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGGCTTG CCGTACCGTC CGGCGGCGCG CGCGGCGCGG
1151 CGGTTGCCTG TGCCGCCTCA TTTTGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCG TTTATATGCA
1251 CACATTGTTT TGCCTGGCCT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGGAA AGATTGTCAC AAAGTGTTC ATTATTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51 SVLCGLDQA YVREYYAAD KDTLFKTLFL PPLLSAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFPIRFL LVLMEGRAL AFSSAQLVSK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPSSAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFVEKTE
401 SSCRWQPLK RPLVMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLGA
451 CILRHRKDLH KLFHYLKKQG FPL*

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a717/m717 97.9% identity in 473 aa overlap

```

a717.pep      10      20      30      40      50      60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCGLDQA
|||||
m717          10      20      30      40      50      60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCGLDQA

a717.pep      70      80      90      100     110     120
YVREYYAADKDTLFKTLFLPPLLSAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE
|||||:|||||
m717          70      80      90      100     110     120
YVREYYATADKDTLFKTLFLPPLLSAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE

a717.pep      130     140     150     160     170     180
LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
|||||
m717          130     140     150     160     170     180
LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA

a717.pep      190     200     210     220     230     240
NLAAAFLLFQNRCRLKAVRRAPSSAVLHRLRYGIPIALSIAWGLASADRLFLKKY
|||||:|||||
m717          190     200     210     220     230     240
NLAAAFLLFQNRCRLKAVRRAPSSAVLHRLRYGIPIALSIAWGLASADRLFLKKY

a717.pep      250     260     270     280     290     300
AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

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|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIENAPPARLSATAESAAALLAS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep  ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
|||||
m717      ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep  LGALAAANLLLLGLAVPSGGARGA AVACASFVWFFVKTESSCRLWQPLKRLPLYMHTLF
|||||
m717      LGALAAANLLLLGLAVPSGGARGA AVACASFVWFFAFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKLFHYLKKQGFPLX
||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLFHYLKKQGFPLX
           430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTGTGG CCGCTGGGCT GGGTCGTTC TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTGG
251 AGCTGTACGG CATGCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCGAAA GCTGGGTGCG CGACAAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLR RENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFRILSWLYM FKHYAVHDFA EFLEYGMPI RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLQMADW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEEDTRE PKDIAVFADA IPKLVDVGVO
251 IPESWVRDKL VIPDVQEGEA VLVRQVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

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1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GGCGGAAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 CGGCGCGCGG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGCGCG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCC ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWRVAPFRN
101 ATPEEKLSD QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFS DGL
151 YLPRNFIHRP QSWFKWDKDN GLLLR TRENP EGEALWPLGW VVHTQKRSV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLLRAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMA DWCEKS
301 AARLILQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGFPLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS DGLYLPRNFIHRPQSWFKWDKDNGLLLRT					
m718	SDGLYVERNFIHRPQSWFKWDKDNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTL SWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTL SWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPF LQMA DW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPF LQMA DW					

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	100	110	120	130	140	150
	300	310	320	330	340	350
a718.pep	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKVAQTITSQIIGPFLQ					
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKVAQTITSQIIGPFLQ					
	160	170	180	190	200	210
	360	370	380	390	400	410
a718.pep	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVGVQIPESWVRDRLVIPDVQEGEA					
m718	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVGVQIPESWVRDRLVIPDVQEGEA					
	220	230	240	250	260	270
	420	430	440	450	460	470
a718.pep	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
	480	490	500	510	520	
a718.pep	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATCGGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAA ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCCGCAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAATGGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAATCCG GAAGCGGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC CGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCGCGACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGGAATC GGTACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCGA CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAA CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGTGTGCG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWVRVAPPRN
101 ATPPEEKLSQ QAYEMMDSL P TLEDLIMDL M DAVGHGFSAL EWEVWVSDGL
151 YLPRNFIHRP QSWFKWDKN D GLLLRTRNP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLRAVEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

```


351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq

1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAACGCGCT GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCCGGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCG CAAAGCTGGT TCAATGGGA
501 CAAAGACAAC GGGCTGTGTC TGCCTACCCG CAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGCGCGCG GCGCAACCAA AGAGGAAAAA
751 AACACCTGTC TTCGAGCGGT GCGGGAATC GGTCAACAAC CGGACGGCAT
801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGCGCGCGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCCGGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCT GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTCCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCGG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHELFDADI EERDSIDIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEELKSD QAYEMMDSL P TLEDLIMDL DAVGHGFSAL EVEVWFSDDL
151 YLPRNFHHRP QSWFKWDKDN GLLRLTREN P EGEALWPLGW VVHTQKRSRV
201 QOARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNNKTKIQKPEAA	LQTDVAQITATGRVIAEHPS	NFITPQKMRA	LFEDAESGDI		
m718-1	MEPIMAKKNNKTKIQKPEAA	LQTDVAQITATGRVIAEHPS	NFITPQKMRA	LFEDAESGDI		
	70	80	90	100	110	120
a718.pep	RAQHELFDADIEERDSIDIAAN	MGTRKRALLTLNWRVAPPRN	ATPTEEELKSD	QAYEMMDSL		
m718-1	RAQHELFDADIEERDSIDIAAN	MGTRKRALLTLNWRVAPPRN	ATPTEEELKSD	QAYEMMDSL		
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSAL	EVEVWFSDDL	YLPRNFHHRP	QSWFKWDKDN	GLLRLTREN	
m718-1	TLEDLIMDLMDAVGHGFSAL	EVEVWFSDDL	YLPRNFHHRP	QSWFKWDKDN	GLLRLTREN	

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	190	200	210	220	230	240
a718.pep	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMP	IRIGK				
m718-1	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMP	IRIGK				
	190	200	210	220	230	240
	250	260	270	280	290	300
a718.pep	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMA	DWCEKS				
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMA	DWCEKS				
	250	260	270	280	290	300
	310	320	330	340	350	360
a718.pep	AARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ	INYP				
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQ	INYP				
	310	320	330	340	350	360
	370	380	390	400	410	420
a718.pep	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDVGVIQIPESWVRDKLVPDVQEGE	AVLVR				
m718-1	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDVGVIQIPESWVRDKLVPDVQEGE	AVLVR				
	370	380	390	400	410	420
	430	440	450	460	470	480
a718.pep	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQ	AVAAL				
m718-1	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQ	AVAAL				
	430	440	450	460	470	480
	490	500	510	520		
a718.pep	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQD	HARAX				
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQD	HARAX				
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1  ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCCGAGATGA
51  CGGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAAATCGCG GCGCAACTT GAACGGCAA GCCATACTTA TGCCTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TGCCTTTAAC CGTTTGCGGC GCAGCGGCAA GGCATCACA AATGATTTGG
251 CACGGGCGGC GGTGCTACG CGTAACCGAA TTCGCGAGCT GAACGCGGAA
301 CTGAAACAGG GCACGGGATT TGCGGACAAG ATGGGAAAAA TCGGAAGATT
351 CGGTGCAGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCAGCGT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTTGGC ACTTGAACCT GTCGAGAAAA
551 ATGGCGGGAC CCACGATAAG GCTTTGGATT TAATCAGCGG CATGATGACC
601 ACCGGTCTGA ATTTGCCCCA AACCAGAAT GAAGCGCAGG CGGCATATGC
651 TTTTGCACTT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AAAGTGATTA
701 AAACCTGAA AGATGGCGGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGTCT TGCAATCGGG TTTAGACGGC ACTTTGAGG TGCGGGATAT
801 GGTTCGGGAG CTGCCGAGCC TGCTCTCTGC CGCGCAACAG GCAGGGATGA
851 ATGGTGTGCG CGGTTTGGAC TACCTGCTCT CACTCTTACA ATCTGCGGCG
901 AATAAATCGG GCAGTCCTGC CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAACT CTGTCGCCTG ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCCGAATGA CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTGTGCAA
1051 GGCAAGCAAA ACGCGCAAAA CGCAGTGCAG GTGTTGTCCC GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTGCAGGCGA TAAGACGGCG GCGGAGCAGG CAAATATGCT TAAGGGCGCG
1201 CTTTGGCGC AACTGCTGCC TGATTGTCAG GCAAAACAAG GTTTGCTGGC
1251 TGCAACGGAT ATGACGCAAA TCCGTGAATA TATGGCTTCG TTGGCTGGCG

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1164

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTCCGCGAGG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTCGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAAA CAACGGTATC CGATTGGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTCACAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CCGTATCAAG TGGCCATGTT
2151 CGGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

```

m719.pep
1  MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51  GIRSEKQIQR EIMLTQAAFN RLARSGKASQ NDLARAATVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLPAMDNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAAYAFAL ASEGSGEDTA KLIKTLKDDG MSGKDLQLGL
251 EHVLSQGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLQSA
301 NKSGSPAEEA TNVONLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKOGLLAATD MTQIREYMAS LAGVTLDNKG IAKNNEARML
451 SAAAQEQEQE SLAMLRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGVVPQYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQOT AAYQAALAOD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

```

m720.seq
1  ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCCG
51  CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCGAGG TGCAGATTAA TCGGGTGTTC TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGGTGC
251 TGGTGCACCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTCCTT GAAAACGCCT
401 TTTTGGTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TCGGGTGTTC GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTTC GAGTGCGGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTTG TTTGATTGTT ACAAAATTGC CTTTCCCGAT
601 CGGGGCGGAT ACAGTGCAGC GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTCATGG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGGTT GGTGCGCCGC ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCGCTATCC CTGATAATT
801 GCTGACCGGC CGCTTTTCAG ACGGCCTGCA AAACCGCCTG AACCGGTTAA

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1165

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CCGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTCGGTGGC AACGGCATT ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCGG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GCGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WKGKYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AEAQEIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNLRL NRLTAKQVQP VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAE SL RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPFIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTGTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TGCGGCGGTC ATCAACCAA AGCCGCGGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCCGCGTT TATCAAGCGC GGCACTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNLRLNRLT AKQVQPVAQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAASGGL TANAVYTEAY QTAESLRAAA
101 GRLNALVAAV INQKPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

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m720 / a720 100.0% identity in 169 aa overlap

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          250      260      270      280      290      300
m720.pep  SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNLRLNRLTAKQVQPVAQAVRLLSTSSLL
          |||||
a720      GLQNLRLNRLTAKQVQPVAQAVRLLSTSSLL
          10      20      30

          310      320      330      340      350      360
m720.pep  SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
          |||||
a720      SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
          40      50      60      70      80      90

          370      380      390      400      410      420
m720.pep  QTAESLRAAAAGRLNALVAAVINQKPPPLIVRQAPIDGTIHQIAHEFYGDIAARAAELVRLNP
          |||||
a720      QTAESLRAAAAGRLNALVAAVINQKPPPLIVRQAPIDGTIHQIAHEFYGDIAARAAELVRLNP
          100      110      120      130      140      150

          430      440
m720.pep  HHHHPAFIKRGTLVNSYAKX

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1166

a720 |||||
 HIHHPAFIKRGTLVNSYAKX
 160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGCCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCGCGCT CGTGAAGGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCGC TGCACTGGCA GGCTCGCAA CGGGCGGCAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGAAGAG GCAGCCGCG
1001 CAAAAATGCT GGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep
1 MSKNAQKLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPWYLTTEE
51 NGHDAVALLN SSRNQLVVDY EHQTLYKEKN GQAPAPAAGWM RWLEFTPCKM
101 FAEVWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON FMKELLQQLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLPQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGCCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCGCGCT CGTGAAGGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCG
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCGC TGCACTGGCA GGCTCGCAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGAAGAG GCAGCCGCG
1001 CAAAAATGCT GGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
  1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTP KGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQOLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLT KYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

	10	20	30	40	50	60
a721.pep	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a721.pep	SSRNQLVVDYEHXTLYKEKNGQPAPAAGWMRWLEFTP KGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHQTLTYKEKNGQPAPAAGWMRWLEFTP KGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a721.pep	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQOLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQOLF					
	130	140	150	160	170	180
	190	200	210	220	230	240
a721.pep	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a721.pep	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI					
	250	260	270	280	290	300
	310	320	330	340	350	
a721.pep	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESGKX					
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
  1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
 51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCTT GATACCGCG ACCGCGAGTA
201 TTGTGAGCGG CATGCCTCCA TCGCGGCTT GAGCCGCCG AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGACCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCACA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGCGGCA AATACCGCA ATCGCCGACG

```

1168

```

401 AGCCGGGCGC GGCCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCGCGCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACGTGTCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

```

m722.pep
1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VDGGAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

```

a722.seq
1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCGC ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGC CGCGGCTT GCGCGCGCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGBA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GGCCGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCGCGCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 CCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACGTGTCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

```

a722.pep
1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCAGC CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGCGAT TTCGTGCGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTGTGTTG
401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTA CTGACC GCCTTGCCTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTCGCGCCA GCCGCCGTC AACAGCAGGC CGCCGCGCCA AAATCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCCT TTTGTCGTCT TCGGCTTTT CCAAGGCTGT GGTGAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTCGGCG GTTTCGTGTT
851 TGTTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1  MRPKPRFRS VIACISVIT PEHLIFTVYK HNTVFARGHF FAAIHAQLH
51  FAFGHSTQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHOR GLCDLAVNQP LVVAVGELQD FQLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARETSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+ 60
TACTCAAATCATTTAACGCTTTTTTTGCCGTGTTTGACGATTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -

CTGCGCGCGGCCCTTTCGGGAAAAATCACGCTGGTGGTGTCTCCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+ 120
GACGCGCGCCGGAAGCCCTTTTGTAGTGCAGACCACAGCAGGCTCGGCTATGTCGCG
a  L R A A F R G K I T L V V S S E P I Q R -

GTGCAGTTGAGCGGCTTGCCGACGAAACCCTGCAAGACCTGAACATTTGCAGGAATAC
121  -----+-----+-----+-----+-----+ 180
CACGTCAAATCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -

GGCTTTGCCAGCCATCCGCCCCACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181  -----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCCGCGTTA
a  G F A S H P P D G S E A V V I P L G G N -
```



```

                ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+-----+ 300
a    TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTCGATGGCGTAGTTTTTGAATTC
    T S H G V I V C S Q H G S Y R I K N L K -

                CCCGGCGAGACGGCGATTTTTAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+-----+ 360
a    GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTAGCACTAATTCGTTCCGTTT
    P G E T A I F N H E G A K I V I K Q G K -

                ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+-----+ 420
a    TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
    I I E A D C D V Y R V N C K Q Y E V N A -

                GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGAGTGTGACGGCGCAA
421  -----+-----+-----+-----+-----+-----+ 480
a    CGGTGCCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACTGCGCGGTT
    A T D A K F N A P L V E T S A V L T A Q -

                GGCCAAATCAACGGCAACGGCGGCATGGCCGTGAGGGCGGCGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+-----+ 540
a    CCGGTTTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAATCG
    G Q I N G N G G M A V E G G D G A T F S -

                GGCGATGTTAACCAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541  -----+-----+-----+-----+-----+-----+ 600
a    CCGCTACAATTGGTTTGGCCGCCGTCGAATTGTGGCTGCCGCTGCACCACCGCCGTTA
    G D V N Q T G G S F N T D G D V V A G N -

                ATATCGTTGCGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601  -----+-----+-----+-----+-----+-----+ 660
a    TATAGCAACGCGGTCGTGGGCGTATGGCTGTCGTAGCCGCGTTTTTGAATGGCCGCTT
    I S L R Q H P H T D S I G G K T L P A E -

                CCGGCATAG
661  ----- 669
a    GGCCGTATC
    P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglIII EcoRI HindIII KpnI NdeI NheI PstI SacI
Sali SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

```

m724.pep
1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGN TSHGVIVCSQ HGSYRIKLNK
101 PGETAIFNHE GAKIVIKQK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTGDGVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

```

a724.seq
1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGCGAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGATCCGG GTTAACGTGA
401 AACAAATACG GGTTAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

```

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
  1 MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
 51 LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQK					
m724	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQK					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
  1 ATGGTGC GCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
 51 GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
101 TTGAGCCTGC CAGCACCGGC GCGGTATGCG GACGTATCA GGATACCGCC
151 GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
201 GCGGCAAGGC GGATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC
251 GCGCTGTTGC CCGCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351 GCAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401 ACACCTGCGG GTTGGAATAT GACCGCTACC CCGAACGCAC CGACAATCCC
451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTTACGAC CCGCAATCCG
551 CCGATGAAT ACCTGTAAAC CTAACCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
  1 MVRTVKS YNG EADDLAQI H TLPVWVTY G GSKVEPAST G GVCGRYQDTA
 51 EFVVMVA ARN LRNEQAQR Q GIDSREIGS N DLIRAVRRL L DGQRLGFADS
101 RGLVPKA VRA IANHVLVQ NA AVSIYAVE YA IRFNTCGLE N DRYPERTDNP
151 DDPNHIF TKY QGTLSEP WPD FEGLDGKI YD PQSADEIPV N LTLKDKQ*

```

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

```
m726.seq
  1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
 51  CCCC GAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101  CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151  GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201  ATGGAAAATC AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251  CCGCCTTGGC ATTCGCGCTC GCGGAAAAGG CGGACGAACT CAAAAACAGC
301  CTCTTGCGCG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351  AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401  TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451  AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCCG GCGCGATTAT
501  CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551  CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601  GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

```
m726.pep
  1  MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
 51  VLTPPRPSDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101  LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVLE
151  KVIEKSARLA VAAGAIIGKR QQLEDKLNLI ETAPGLDALE KEIEEWTLNI
201  G*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

```
a726.seq
  1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
 51  CCCC GAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101  CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151  GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201  ATGGGAAATC GCGGAAGCCG CTGCGCGCCG CCGTTTCGCC GAACAAAAAA
251  CCGCCACGGC ATTCGCGCTC GCGGCAAAGG CGGACGAACT CAAAAACAGC
301  CTCTTGCGCG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351  AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401  TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451  AAAGTTGTCT AAAAATCCGC CCGCCTGGCC GTTGCCGCCG GCGCGATTAT
501  CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551  CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601  GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

```
a726.pep
  1  MTIYFKNGFY DDTLGSIEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
 51  VLTPPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101  LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVLE
151  KVIEKSARLA VAAGAIIGKR QQLEDKLNLI ETAPGLDALE KEIEEWTLNI
201  G*
```

a726/m726 95.5% identity in 201 aa overlap

```

          10      20      30      40      50      60
a726.pep  MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPPRPSEY
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m726      MTIYFKNGFYDDTLGGIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPPRPSDY
          10      20      30      40      50      60
```

m727.seq

```
1 ATGAATCTCG TGAAACTGCT GCGCAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAAG
101 CGGCATTTCG GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTGTGC GGCTCAAAAC TATGCGCGCG AACTGGAAAG
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTCTCGGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTTAA
```

m727.pap

1	MNLVKLLANN	WQPIAIIALV	GTGLAVSHHQ	GYKSAFAKQO	AVIDKMERDK
51	AQALLLSAQN	YARELELARA	EAKKYEVKAH	AVGMALAKKQ	AEVSRLKTER
101	DLCKIPFPDP	SRNPNTGFRL	FSPQIPPNFT	QIPP*	

a727.seq

```
1 ATGAATCTCG TGAACTGCT GCGCAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGT TGGCGGTGTC GCACCATCAA GGCTACAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAATGTAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCGCCGC AACTGGAACA
201 GCGCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAATTAA
```

a727.pep

1	MNLVKLLANN	WQPIAIIALV	GTGLAVSHHQ	GYKSAFAKQQ	AVIEKMKRDK
51	AQALLLSAQN	YARELEQARA	EAKKYEVKAH	AVGMALAKKQ	AEVSRLKTEN
101	KKEIENVLTQ	DRKNAGGGCI	DGFGHHGLQL	YKRALGYGN*	

a727.pep MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSFAFAKQQAIVIEKMKRDKAQALLSAQN
| | | | | | | | | | | | | | | | | | | | | : | | | | |

1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQYKSAFAKQQAVIDKMERDKAQALLLSAQN
           10      20      30      40      50      60
           70      80      90      100     110     119
a727.pep  YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAEAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDPSRNPNTGTF
           70      80      90      100     110
           120     130     140
a727.pep  IDGFGHHGLQLYKRALGYGNX
m727      RLFSPPQIPPNTQIPPX
           120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTGCTTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACGGGATG GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTT
901 ATTGCACAAT CTTGACGCGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGATG GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

```

g728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQ AQVYLAKYRD VANDEQKVD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

```

m728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAATG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTGCTTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

```

501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GAAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG CGGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACG AAATCTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GGCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAATAAT TGGAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

```

m728.pep
  1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
 51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHLGICYQM AQVYLAKYRD VANDEQKVD FRKESNRIAS DSRNSVIFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS FDNGKKRQSF EYYLKNLNF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

m728.pep	10	20	30	40	50	60
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNNAFVAKLARLFRNA					
g728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPDGSVFDAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVD FRKESNRIAS					
g728	WQPDGSVFDAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVD FREESNRIAS					
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSVIFYQNMRELMPRGMKANSLVVGIDADGLPQKVYWSFDNGKKRQSFEYYLKNLNF					
g728	DSRDYVIFYQNMRELMPRGMKANSLVVGIDADGLPQKVYWSFDNGKKRQSFEYYLKNLNF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

1176

```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360

           370
m728.pep  YAEAAARRSGRRDL SHX
           |||||
g728      YAEAAARRSGRRGL SHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAAACTT
151 GCCCGCTGT TCCGAAATGC CGACAGGCGG GTTGTTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGCGCG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCCGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCAGGTA TATTTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCGCGGAA GAGAGTAACC
701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTGAA CTGGAAGAT
1051 TTGAAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHEGEVWLD YYIGEGGLVA VLSLSQSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LUVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

a728 / m728 96.3% identity in 377 aa overlap

```

           10      20      30      40      50
a728.pep  MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10      20      30      40      50      60

           60      70      80      90      100     110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYALAVRLSRLKEKAKWFHVTEQEHEGEEV
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYALAIRLSRLKEKAKWFHVTEQEHEGKEV
           70      80      90      100     110     120

           120     130     140     150     160     170
a728.pep  WLDYYIGEGGLVAVSLSQSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV
           ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      WLDYHIGEGGLVAVSLSQSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV
           130     140     150     160     170     180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDAASGRGKIGEDVYEHCLGQYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDAAGRGKIGEDVYEHCLGQYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
a728.pep	240	250	260	270	280	290
	DSRDSVIFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFYEYLLKNGNLF					
m728	DSRNSVIFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFYEYLLKNGNLF					
	250	260	270	280	290	300
a728.pep	300	310	320	330	340	350
	IAQSSSTVALKADGVTADMQTYHAQQTWYLDGGGRIVREEKQGDRLPDFPLNLEDEKEVSR					
m728	IAQSSSTVALKADGVTADMQTYHAQQTWYLDGGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
a728.pep	360	370				
	YAEAAAARRSGGRRDLSHX					
m728	YAEAAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTCTGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTTCCAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCgg
351 caaTGTCAGC AGCAGCTACA ATGTCGGACT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgCGATGCG GCACATTTGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgaTgT
551 CTTTGGGCGCa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTGCGGT ACAAGGCAGG CGTGATTTCG GCGTTCGCCC TCGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
701 gcCGCGAACA GGCGCGCAAT GCCTTGCGAA CCTTGATTAA ccGTCCGATA
751 CCCGAaagcC TGCCCGCCGG TTTGCCGTTG GACAagcAGT TTTTGTGTA
801 AAAACTGCCT GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCCGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCGTGC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GCGGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATT TTAATTGGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCCAA CAGGCACAAA TTGTGCTTA
1101 TGAATCCGCC GTCCAATCCG CCTTCAAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGATTGCG TCGATGCGGA ACGCATCAGC TATTGCGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDYFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEALQG
151 YFASVANRDA AHLILIATVA KAYFNERYAE KAMSLAQRVL KTREETYKLS

```


m729.seq

m729.pcp

m729.pep MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g729 MNNTTLKTTLTLSVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDYFAD
 10 20 30 40 50 60

1179

	70	80	90	100	110	120
m729.pep	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNVS					
g729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANGSRQGSLSGGNVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVLGAASYELDLFGRVRSSEAAALQGYFASTANRDAHLSLIATVAKAYFNERYAE					
g729	SSYNVGLGAASYELDLFGRVRSNSEAAALQGYFASVANRDAHLILIATVAKAYFNERYAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRVLKTREETYKLSERYKAGVISAVALRQOEALIESAKADYAHAAARSREQARN					
g729	KAMSLAQRVLKTREETYKLSERYKAGVISAVALRQOEALIESAKADYAHAAARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTGTVGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	ARAAFFPSIRLTGTVGTGSAELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
g729	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQTKX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC
51  ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGC GGTC
151 GATTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGC GGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTCGCCA GCACCGCCAA CCGCGATGCG GCACATTTGA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGGCGCA ACGTGTTTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTCG GCCGTCGCCC TACGTCAGCA
651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTGCAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCGCGCGG TTTGCCGTTG GACAAGCAGT TTTTGTGTA
801 GAAGCTGCCG GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCGC CCTTTTCC ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GCGTGTGGT
1001 TGTCGCACC TTCCATTACC CTGCCGATT TTACCTGGGG TACGAACAAG

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1180

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1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

```

a729.pep
  1  MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
 51  DLGWHDFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNLLP
101  TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RSSSEALQG
151  YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201  ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251  PDDLPAGLPL DKOFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301  ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351  ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401  ASKEALRLVG LRYKHGVSGA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451  LYKALGGGLK RDTQTDK*

a729 / m729    98.1% identity in 467 aa overlap

      10      20      30      40      50      60
a729.pep  MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD
          |||
m729      MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD
      10      20      30      40      50      60

      70      80      90     100     110     120
a729.pep  PRLQKLIDIAL ERNTSLRTA VLNSEIYRKQ YMIERNLLPT LAANANDSR QGSLSGGNVS
          |||
m729      PRLQKLIDIAL ERNTSLRTA VLNSEIYRKQ YMIERNLLPT LAANANDSR QGSLSGGNVS
      70      80      90     100     110     120

      130     140     150     160     170     180
a729.pep  SSKVGLGAAS YELDLFGRV RSSSEALQGY FASTANRDA AHLSLIATVAKAYFNERYAE
          |||
m729      SSKVGLGAAS YELDLFGRV RSSSEALQGY FASTANRDA AHLSLIATVAKAYFNERYAE
      130     140     150     160     170     180

      190     200     210     220     230     240
a729.pep  EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
          |||
m729      EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
      190     200     210     220     230     240

      250     260     270     280     290     300
a729.pep  ALATLINQPI PDDLPAGLPLDK OFFVEKLPAGLSSEVLLDR PDIRAAEHALKQANANIGA
          |||
m729      ALATLINQPI PEDLPAGLPLDK OFFVEKLPAGLSSEVLLDR PDIRAAEHALKQANANIGA
      250     260     270     280     290     300

      310     320     330     340     350     360
a729.pep  ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNKANLDVAKLRQ
          |||
m729      ARAAFFPSIR LTGTGTGS AELGGLFKSGTGVWSFAPSITLP IFTWGTNKANLDVAKLRQ
      310     320     330     340     350     360

      370     380     390     400     410     420
a729.pep  QAQIVAYEAA VQSAFQDVAN ALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA
          |||
m729      QVQIVAYESA VQSAFQDVAN ALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA
      370     380     390     400     410     420

```

1181

	430	440	450	460
a729.pep	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	:			
m729	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

```

1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GGC GGTGCGA  CTCATACAGC  CCGCCCTCGC  GCGGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACACC  CAACGGCAGC  ACTACGAACC  CGGCGGCAAA
151 TACCACCTCT  TCGGcgaCCC  GCGCGCAGC  GTTTCGACC  GCACCGGCAA
201 AATCAACGTC  ATCCAAGACT  ATACCACCA  GATGGCAAC  CTGCTCATCC
251 AACAGGCGGC  AATCCAAGGC  AATCTTGTT  ACACCGTCCG  CTTTCCGGA
301 CACGACACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 AAGCGAAGAA  AAAGCAACG  TTGACGACGG  CTTTACCGTG  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGGCAATT  ACCCAAACC  TACGGGCGCA  CGAGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCCGCA  GTATCAAACT  CAATCCGACC  GACACCGGCA
551 GCATCCGGCA  ACGCATATTC  GACAACTACA  ACAACCTCGG  CAGCAATTTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TGTCAACGGC  GTCGCCGCCG
701 AGCGGCTCAA  CCCCTTTATC  AGCGGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCGA  TCGCGAACAT
801 CGCCCCCTTA  CCCGCCGAGG  GCAAATTCGC  CGCCATCGGC  GGCTTGGGCA
851 GCGCGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GCGGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  TGGGGATTTT  TCTAAATCCT  ACACCTGCTC  CTTCCACGGC
1051 AGCACCTTGG  TCAAACGGC  AGACGGCTAC  AAAGCCATTG  CCCATATTCA
1101 AGCCGGAGAC  CGCGTCTTT  CCAAGGACGA  GGCAAGCGGA  GAAACGGGAT
1151 ACAAAACCGT  TACCGCCCGA  TACGGCAATC  CGTATCAAGA  AACCCTTAC
1201 ATTGAAGTTT  CAGACGGCAT  CGGCAACAGC  CAAACCCTGA  TTTCCAACCG
1251 CATCCACCGG  TTTTATTCGG  ACGGCAATG  GATTAAGGCG  GAAGATTAA
1301 AAGCGGGAAG  CCGGCTGTTA  TCCGAAAGCG  GCAAAACCCA  AACCCTCCGC
1351 AACATCGTTG  TCAAACCAA  ACCGCTCAA  GCCTACAATC  TGACCGTTGC
1401 CGATTGGCAT  ACCTACTTCG  TCAAGGTA  TCAGGCGGAA  ACGGAAGGGG
1451 TTTGGGTTCA  TAATGATTGT  CCGCCTAAAC  CAAAACCAAC  CAATCATGCC
1501 CAACAAAGAA  AAGAAGAAGC  TAAAAACGAT  TCTCATCGAA  GTGTGGGAGA
1551 TTCCAATCGT  GTCGTTGCGG  AAGGAAAGCA  ATATTAGAT  TCCGACACAG
1601 GAAACCATGT  TTATGTAAAA  GGAGATAAAG  TGGTTATTCT  AACTCCTGAT
1651 GGAAGACAGG  TAACTCAATT  TAAGAACTCG  AAAGCCAATA  CGTCAAAAG
1701 GGTAAAAAAT  GGGAAATGGA  CACCAAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

```

1  VKPLRLRLTNL  LAACAVAAVA  LIQPALAADL  AQDPFITDNT  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGKINV  IQDYTHQMG  LLIQQAIIQG  NLGYTVRFSG
101 HGHEEHAPFD  NHAADSASEE  KGNVDDGFTV  YRLNWEGHEH  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIF  DNYNNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNMSEFVNG  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAAIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVKNLTKAAK  PGKAAVSGDF  SKSYTCSFHG
351 STLVKTAGDY  KAIAHIQAGD  RVLKDEASG  ETGYKPV TAR  YGNPYQETVY
401 IEVSDGIGNS  QTLISNRIHP  FYS DGKWIKA  EDLKAGSRL  SESGKTQTVR
451 NIVVKPKPLK  AYNLTVADWH  TYFVKGNAE  TEGVWVHND  PKPKPTNHA
501 QQRKEEAKND  SHRSVGDSNR  VVREGKQYLD  SDTGNHVYVK  GDKVVILTPD
551 GRQVTQFKNS  KANTSKRVKN  GKWTPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

```

1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGCGCGCA  CTCATACAGC  CCGCCCTCGC  GCGGACTTG  GCGCAAGACC

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1182

```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTCCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCGCGG ATGCCTACGA CGGCCCGAAG
451 GCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC CTCGCCGCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATCTT ATAAAAAGAA ATTGGCTTTG
1051 TGTGATAGTG CGAGACAGTT ATATCAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCAAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AAGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTC TTCACAAGTT
1351 AAGTCATATA TTGAATCAAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1 VKPLRLRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51 YHLFGDPRGS VSDRTGKINV IQDYTHQMG NLLIQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADENRKM FEHNAKLDR WGNMSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPFNFLNQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

```

          10      20      30      40      50      60
g730.pep  VKPLRLRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VKPLRLRLTNLLAACAVAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS
          10      20      30      40      50      60

          70      80      90      100     110     120
g730.pep  VSDRTGKINVIQDYTHQMGNLLIQAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE
          70      80      90      100     110     120

          130     140     150     160     170     180
g730.pep  KGNVDDGFTVYRLNWEGHEHHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      KGNVDEGFTVYRLNWEGHEHHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT
          130     140     150     160     170     180

          190     200     210     220     230     240
g730.pep  DTRSIRQRIFDNYNNLGSNFSADRAENRKMFEHNAKLDRWGNMSEFVNGVAAGALNPFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      DTRSIRQRISDNYSNLGSNFSADRAENRKMFEHNAKLDRWGNMSEFINGVAAGALNPFI
          190     200     210     220     230     240

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1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
	: : :					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAAKPGKAAVSGDFSYSYTCSEFHGSTLVKTADGY					
	: : :					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAGKPGKAAVSGDFADSYKKKIALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVNTARYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRKTDGSSKFINGREIDAVTNDALIAQKRTISAIDKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TCGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GGGCGCCGCA  CTCATACAGC  CCGCCCTCGC  GGGCGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGCGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTCCGGA
301 CACGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCGCGCG  ATGCCCTACG  CGGCCCGAAG
451 GGGCGCAATT  ACCCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCAGCGA  GCATCAAAT  CAATCCGACC  GACACCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCCCGCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TCGGCAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTCGC  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCCG  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAAC TAGA
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAAT  AGAATCAGAC  AGAACCAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCGTATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAAC TG
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRLRIKL  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGVEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRI  DNYSNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNSEEFING  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSVAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTAAK  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRQNQKNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGDE
401 AGGGHLFPGK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARVW  SYETRDGIRI  RTVYEPATGK  VVTAFPDRTS  NPKYNPVK*

```

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRRLIKLLAACAVAAAAALIQPALAADLAQDFFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAAAALIQPALAADLAQDFFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730.pep	DTRSIRQIRISDNYSNLGNSFSDRADEANRKMFEHNAKLDRWGNSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGNSFSDRADEANRKMFEHNAKLDRWGNSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAPGKAAVSGDFSAAYNTRTRKVTETETGLN					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730.pep	RIRQNQKNSNIHEKNYGRDNPNNHINVLSGNSIQHILYGDEAGGGHLFPKGKPTTFPQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIIDKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gattttcgag cgttttcatG CGAGAACGGT TTGTCTGTGC GCGTCCGCAA
51  TTTGGACGGC GGCAAAATCG CGTTGCGGCT GGACGGCAGG CGTGCCGTCC
101 TCTCTTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT
151 TTGTTTCGAA ACGGAACCGA GTGGCACCAG AAAGGCGGCG AAGCCTTTT
201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAAACTTCC TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG LSVRVRLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG
51  LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGCGGGC
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCCTGCGAG
151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT
201 GCGGCTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG

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251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CACCAGAAAG GCGGCCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep
 1 MNIRFFALTV PVL~~SLA~~ACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
 51 NGLSVRVRL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

g731/m731 95.2% identity in 84 aa overlap

g731.pep					10	20	30
					DFRAFS	ENGLSV	RVRNLDG
m731	LSLAACAV	PEAYDDGGRG	HMPPVQNQAG	TDDFRAFS	ENGLSV	RVRHLD	DSGKVALRLDGR
	20	30	40	50	60	70	

g731.pep					40	50	60	70	80
					RAVLSSD	VAASGERY	TAEHGLFG	NGTEWHQK	GGGEAFFG
m731					RAVLSSD	VAASGERY	TAEHGLFG	NATEWHQK	GGGEAFFG
					80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq
 1 ATGAATATCA GGT~~TTTT~~TCGC GCTGACCGTA CCGGTTTGT CTTGGCGGC
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CCGACGAGGG CATATGCCGC
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTG GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGG AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep
 1 MNIRFFALTV PVL~~SLA~~ACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

a731/m731 94.4% identity in 126 aa overlap

a731.pep					10	20	30	40	50	60
					MNIRFF	ALTVPV	L SLA ACAV	PEAYDDGGRG	HMPPVQNQAG	TADFRAFS
m731					MNIRFF	ALTVPV	L SLA ACAV	PEAYDDGGRG	HMPPVQNQAG	TDDFRAFS
					10	20	30	40	50	60

a731.pep					70	80	90	100	110	120
					DGGRIAL	RLDGRRA	VLSSDVA	ASGERYTA	EHLFGNG	TEWHQKGG
					::	::	::	::	::	::
m731					DSGKVAL	RLDGRRA	VLSSDVA	ASGERYTA	EHLFGNA	TEWHQKGG
					70	80	90	100	110	120

a731.pep	TSCRARX
m731	TSCRARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq
 1 ATGTCGAAAC CTGTTTTTAA GAAATCGCA CTTTACTT TGGGTGCAAT
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtC CTGCCGGTGC AATCCATCCG TACGATGGCG


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151 GAGGTTTACG GTCAGATTAA GGCAAACACTAC TATCATGACA AACCCGATGC
201 CGATTGTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTGCGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCTGCGCG AGTTGAAAAC GATTCCGATG ACGgtatTGG TcaaTTCCGG
951 TTCggttCC GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTACGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGGACCTG
1201 GTCGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAC
1251 CCTtgcCGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732.pep

```

1 MSKPVEFKKIA LYTLGAISGV AVSLAVQGFA AEKDGDRNEV LPVQSIRTMA
51 EVYGGQIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGyAEIKEST
101 SGFEFGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGYIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSAE FLPSEAVVVS TKGRDGKDDM VLKAVPEDYV YGMGGDPLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFQKGSVQT
351 LIPLNSGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDAKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKKKD K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732.seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGCGGTG GCCGTGAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGTGTC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACACTAC TATCAGGACA AACCCGATGC
201 CGATTGTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTGCGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCATTCTCTA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCTGCGCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGCTTCC GCGTCGGAGA TTGTCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

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1187

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1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTTG
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGCTTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGGIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKS GDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAII KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA A FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLGA
301 IPAEKLTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKDADKPA VKEGKKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKKKD KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGGIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGGIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	:					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m732.pep	VSPIEDTPAERAGVKS GDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIEDTPAERAEVKS GDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLGA					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m732.pep	KLTTALYYTTPNDRSIQAQGI VPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
g732	KLTTALYYTTPNDRSIQAQGI VPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
g732	PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVSNDKKDKDKKX					
g732	PVSNDKKDKDKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

a732.seq

1	ATGTCGAAAC	CTGTTTTTAA	GAAAATCGCA	CTTTATACTT	TGGGTGCAAT
51	CAGCGGCGTG	GCCGTCAGTC	TGGCGGTGCA	GGGTTTGGCC	GCCGAGAAGG
101	ACAGGCGGGA	TAACGAAGTC	CTGCCGGTGC	AATCCATCCG	CACAATGGCG
151	GAGGTTTACG	GTCAAATCAA	GGCAAACCTAC	TATCAGGACA	AACCCGATGC
201	CGATTTGTTT	GAAGGTGCGA	TGAAGGGTAT	GGTGGCCGGT	TTGGATCCGC
251	ATTCGGAATA	TATGGATAAA	AAAGGTTATG	CCGAGATAAA	GGAGTCCACC
301	AGCGGCGAAT	TTGGCGGCTT	GGGGATGGAA	ATCGGGCAGG	AAGACGGATT
351	TGTCAAAGTG	GTTTCGCCGA	TTGAGGACAC	GCCTGCGGAA	CGGGCGGGGG
401	TGAAAGCGG	CGATTTTCATT	GTGAAAATCG	ATAATGTTTC	GACACGCGGC
451	ATGACGGTCA	GCGAAGCGGT	GAAGAAAATG	CGGGGCAAGC	CGGGTACGAA
501	GATTACTTTG	ACGCTGTTCG	GCAAAAATGC	CGACAAGCCG	ATAGTCGTCA
551	ACCTGACCCG	TGCCATTATT	AAAGTGAAAA	GCGTCCGCCA	TCACCTGATC
601	GAACCCGATT	ACGGCTATAT	CCGCGTGTCT	CAGTTCCAAG	AGCGGACGGT
651	CGAAAGCGTC	AATACCGCCG	CAAAAGAGCT	GGTAAAGGAA	AATAAAGGAA
701	AACCGCTCAA	GGGGCTGGTG	TTGGATTGCG	GCGACGACCC	CGGCGGGCCT
751	TTGACTGGCG	CGGTGCGCGT	GTCGGCGGCA	TTTCTGCCGT	CTGAAGCAGT
801	CGTCGTCAGC	ACCAAGGGAC	GCGACGGCAA	AGACCCGATG	GTAAGTAAAG
851	CCGTTCCTGA	AGATTATGTG	TACGGGATGG	GCGGCGATTG	GTTGGCGGGC
901	ATTCCTGCCG	AGTTGAAAAC	CATACCGATG	ACGGTATTGG	TCAATTCGGG
951	TTCCGCTTCC	GCGTCGGAGA	TTGTGCGCAG	TGCATTGCAG	GATCATAAAC
1001	GCGCGGTCAT	CGTCGGTACG	CAGAGCTTCG	GCAAAGGTTT	GGTTCAGACT
1051	TTGATTCCCT	TGTCCAACGG	CAGCGCGGTC	AAGCTGACAA	CGGCACTGTA
1101	TTATACGCCG	AACGACCGTT	CTATTCAGGC	GCAGGGGATT	GTTCCCGATG
1151	TCGAAGTAAA	AGATAAGGAA	CGCATTTTTG	AAAGCCGCGA	GGCGGATTTG
1201	GTCGACACA	TCGGCAATCC	TTTGGGCGGC	GAGGATGTGA	ACAGTGAAAC
1251	CCTTGCCGTG	CCGCTTGAAA	AAGATGCGGA	TAAGCCCGCT	GTAAGAGAAA
1301	AAGGTAAAAA	GAAAAAGGAC	GAGGATTTGT	CTTCAAGGCG	GATTCCCAAC
1351	CCTGCCAAAG	ACGACCAGTT	GCGGAAAGCT	TTGGATTAG	TCAAGTCGCC
1401	CGAGCAGTGG	CAGAAGTCTT	TGGGGCTGGC	GGCGAAAAAG	CCGTTTCAA
1451	ATAAGATAAA	GAAAGATAAA	AAAGATAAGA	AGTAG	

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

a732.pep

1	MSKPVFKKIA	LYTLGAISGV	AVSLAVQGFA	AEKDRRDNEV	LPVQSIRTMA
51	EVYGOIKANY	YQDKPDADLF	EGAMKGMVAG	LDPHSEYMDK	KGYAEIKEST
101	SGEFGGLGME	IGQEDGFVKV	VSPIEDTPAE	RAGVKSDFI	VKIDNVSTRG
151	MTVSEAVKKM	RGKPGTKITL	TLSRKNADKP	IVVNLTRAI	KVKSVRHHLI
201	EPDYGIRVS	QFQERTVESV	NTAAKELVKE	NKGKPLKGLV	LDLRDDPGGL
251	LTGAVGVSA	FLPSEAVVVS	TKGRDGKDRM	VLKAVPEDYV	YGMGGDSLGA
301	IPAEIKTIPM	TVLVNSGSAS	ASEIVAGALQ	DHKRAVIVGT	QSFKGSVQ
351	LIPLSNGSAV	KLTTALYYTP	NDRSIQAQGI	VPDVEVKDKE	RIFESREADL
401	VGHIGNPLGG	EDVNSSETLAV	PLEKDADKPA	VKEKGKKKKD	EDLSSRRIPN
451	PAKDDQLRKA	LDLVKSPEQW	QKSLGLAAKK	PVSNKDKKDK	KDKK*

1189

a732/m732 99.6% identity in 494 aa overlap

	10	20	30	40	50	60
a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYQGQIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYQGQIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
a732.pep	IVVNLTRAIKVKSVRHHLLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
a732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG					
m732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
a732.pep	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
m732	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360
	370	380	390	400	410	420
a732.pep	KLTTALYYTPNDRSIAQGGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	KLTTALYYTPNDRSIAQGGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
	430	440	450	460	470	480
	490					
a732.pep	PVSNDKKDKKKKX					
m732	PVSNDKKDKKKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGTT TGAAAAACGa cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCC CGGGTGCGCA CGCCCATTTG GGACTGCTGC

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1190

251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDTTS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CCGGTGCGCA CGCCCATCTG GGA CTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTLSRL SLCAAVLALT ACGNGQKSL YYYGGYPDTV YEGLKNDTTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDTSLGKQTEKMEK					
g733	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDTSLGKQTEKMEK					
	10	20	30	40	50	60
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
g733	YFAEAANKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CCGGTGCGCA CGCCCATCTG GGA CTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

```

1  MMNPKTL SRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
51  LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

              10      20      30      40      50      60
a733.pep      MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLNDDTSLGKQTEKMEK
              |||||
m733          MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLNDDTSLGKQTEKMEK
              10      20      30      40      50      60

              70      80      90      100     110     120
a733.pep      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERKLFPESGVFMDFLMKTGKG
              |||||
m733          YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERKLFPESGVFMDFLMKTGKG
              70      80      90      100     110     120

a733.pep      GKRX
              ||||
m733          GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTTG CAGGTAAAA CCACAAAAGA AGATTCCGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCC TTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GAAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
451 GCTGTTGCTT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
1  MMKKILAVSA LCLMTAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHQQV ALNQCIKKYG AQGQCGLTV YCTSSSYGG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTGCTG
51  GAACAATACC TGTGTCGCGC TGGCATAACC GAAAGCCTTG GGCGCGCTGC
101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCAAGT CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGGA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAACGT
251 TCGGCTCTTT GATTCAAAAT CTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSVLNNT CVALAYPKAL GALRVDNAV VITS PRFTSVH
51  QVALNQCIKK YGVQGCGLT TVYCTSSSY GGTVRS LIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

              10      20      30
m734.pep      SGIAEDEPTGCRSVVSLNNTCVALAYPKAL
              :|||
g734          VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL

```

1192

	40	50	60	70	80	90
m734.pep	GALRVDNAVVITSPRFTSVHQAVALNQCIKKYGVQGCGLQETVYCTSSSYGGTVRSLIQN					
g734	GAMRVENAVVITSPRFTSVHQAVALNQCIKKYGAQGCGLQETVYCTSSSYGGAVRSLIQH					
	100	110	120	130	140	150
m734.pep	LKX					
g734	LKX					
	160					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2497>:

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGACTGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTGT CAGGTTAAAA CCACAAAAGA AGATTGACG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCT TTCTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCTCAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 2498; ORF 734.a>:

```
a734.pep
1  MMKKILAVSA LCLMTAAARA ADTYGYLAVW QNPQNANDVL QVKTTKEDST
51  KSEAFAELEA FCKGQDTLAG IEDEPTGCR SVVSLNNTCV ALAYPKALGA
101 MRVENAVVIT SPRETSVYQV ALNQCIKKYG AQGCGLQETV YCTSSSYGG
151 TVRSLIQNLK *
```

a734/g734 95.6% identity in 160 aa overlap

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQA					
	70	80	90	100	110	120
a734.pep	ALNQCIKKYGAQGCGLQETVYCTSSSYGGTVRSLIQNLKX					
g734	ALNQCIKKYGAQGCGLQETVYCTSSSYGGAVRSLIQHLKX					
	130	140	150	160		

g735.seq not found yet
g735.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2499>:

```
m735.seq
1  ATGAATCTCG TGAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51  CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAGT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGAAAAAT
301 AAAAAGGAAA TCGAAATGT CTTACTCAA GACCGTAAAA ATGCAAGCGG
```

1193

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GCGCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735						
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735						
	70	80	90	100	110	120
	130	140				
a735.pep	DFGHHGLQLYKRALGYGNX					
m735						
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGCG
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTG TCGETATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCAGCAACT GGGTCCCCTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCC CGCGTTTTTG GCGGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCTGTA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAAACAC ATTACGATAC ATTACGATGT AATCAACGGT

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSFGS ITLFLNILA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHVDVING
 201 LIKSAAFGVA VTLLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCGGCAGT ATCAGCGTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
 151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCG TCGGTATGGT
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATCAAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGC CGCAACT GGGTCCCGTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCG CGCGTTTTTG GCGGGGCGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
 551 GGCCGCAGAT GCAGAACAAAC ATTACGATAC ATTACGATGT AATCAACGGT
 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMNN ITIHVDVING
 201 LIKSAAFGVA VTLLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	: : : :					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNILAKSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	: : : :					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
	: : :					
g736	MKTTGQLEAMNVMAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

1195

	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
g736	GIFWPMQNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCIPPTSEGILRASTRTVVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

1	ATGAATTTTA	TCCGTTCCTG	CGGGGCGAAA	ACCCTCGGCC	TTATTCAATC
51	TCTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	TATTCTGGCG	AAATCCGGTA
101	CGGCTTTCGT	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	TTTTGCCGGC
151	GTGCTGTGG	TGTTGATTGT	TGCCGTTTCA	GGGCTGTTTG	TCGGCATGGT
201	CTTGGGTTTG	CAGGGCTATA	CGCAGTTGTC	GAAATTCAAA	TCCGCCGATA
251	TTTTGGGCTA	TATGGTCGCG	GCTTCGCTGT	TGCGCGAACT	GGGTCCGGTG
301	TGGCGGCGCA	TTCTGTTTGC	CAGCAGCGCG	GGCGGTGCGA	TGACCAGCGA
351	AATCGGTTTG	ATGAAAACGA	CCGAACAGCT	CGAAGCGATG	AACGTGATGG
401	CGGTAAACCC	CGTCGCCCGA	GTGTTGCGC	CGCGCTTTTG	GGCGGGCGTG
451	TTTTCATGCG	CGCTTTTGGC	TTGATTTTTC	AACGTGGCGG	GTATTTTCGG
501	CGCGTATTG	GTGCGTGTA	CCTGGCTGGG	CTTGGACAGC	GGTATTTTCT
551	GGTCGCAAT	GCAGAACAC	ATCACGATAC	ATTACGATGT	AATCAACGGT
601	CTGATCAAAT	CCGCCGCGTT	CGGCGTGGCG	GTAACGCTGA	TTGCCGTGCA
651	TCAGGGCTTC	CACTGCGTCC	CGACCTCGGA	AGGCATTTTG	CGCGCCAGCA
701	CGCGCACGGT	GGTTTCGTCC	GCCCTGACGA	TTTTGGCGGT	CGATTTTATA
751	TTGACCGCGT	GGATGTTTAC	AGATTGA		

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

1	MNFIRSVGAK	TLGLIQSLGS	ITLFLNILA	KSGTAFVRPR	LSVRQVYFAG
51	VLSVLIVAVS	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELGPV
101	LAAILFASSA	GGAMTSEIGL	MKTTEQLEAM	NVMAVNPVAR	VVAPRFWAGV
151	FSMPLLASIF	NVAGIFGAYL	VGVTWLGLDS	GIFWSQMNN	ITIHVDVING
201	LIKSAAFGVA	VTLIAVHQGF	HCVPTSEGIL	RASTRTVVSS	ALTILAVDFI
251	LTAWMFTD*				

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWLGLDS					
m736	MKTTEQLEAMNVMAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWLGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					

1196

```

m736      GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep  ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

```

g737.seq
1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

```

g737.pep
1  MNIKHLLLTA AATALLGISA PALAHHDGHC DDDHGHAHQ HGKQDKIISR
51 AQAEKAARAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

```

m737.seq
1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

```

m737.pep
1  MNIKHLLLTS AATALLSISA PALAHHDGHC DDDHGHAHQ HNKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

```

m737/g737
           10      20      30      40      50      60
m737.pep  MNIKHLLLTSAATALLSISAPALAHHDGHDGDDHGHAHQHNKQDKIISRQAQEKAALAR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g737       MNIKHLLLTAAATALLGISAPALAHHDGHDGDDHGHAHQHGKQDKIISRQAQEKAARAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||
g737       VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

1197

```

a737.seq
1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACA ACGGCGGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

```

a737.pep
1  MNFKRLLLLTA AATALMGISA PALAHHDHGHG DDDHGHAHQ HSKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLLTA	AATALMGISA	PALAHHDHGHG	DDDHGHAHQ	HSKQDKIISR	AQAEKAALAR
m737	MNIKHL	LLTSAATALLS	ISAPALAHHDHGHG	DDDHGHAHQ	HNKQDKIISR	AQAEKAALAR
	10	20	30	40	50	60
	70	80	90	100	109	
a737.pep	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
m737	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

```

g738.seq
1  ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCGC CAAACTGCCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCGGCCGCGC TGATTGTCTC GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGGCT TCAGGCAGCG CTGATGAACC TGATTTATCC CGGAATGAAC
301 GACATCGCCT CTTGGGTTT CATCTTGCTC GCCGTGACG CGTGGGCGCTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCATcgtT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCTCTG CTTCAAAACA TCATCGTTCA
501 CAGAGGGCAA GCGGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC GCCATTCTGG AACCTTTTAC AGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATCGGGCA
951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATACA CGACAACCTC CTCAGCACCT TGTTACCCCA TTCCACAAC
1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTTCTCT CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTCTCG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCC GCCGCT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAATA CCGCCCTAC TCCGCCACCT

```

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1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAACA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

```

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51 AAGLIVLLEFL TAGKKLFDVK IPAISFLLEFA MAFFWLQAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAAFQ SAPIFGHWGN SFAQOTFLIN AEQHTIHDNF LSTLFTSHSN
351 IILQLLAEMG ISGTLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALEPY PETQTWAEAA TLKALKYRKY SATYRIALYL MRQKVAEAK
551 QWMRTQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCCKA FAAAPGHPET
601 KPKC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

```

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCGG CCAAAGTCCC
51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGGCC TGATTGTCCT GTTGTTCTCT ACGGCAGGAA AAAAAGTGT
201 TGATGTCAA ATCCCGGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCGCTG
351 CCGGAGCTTG GTCGCACTCT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATCGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCCGCG CTAACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCGAAT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGTCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTACCCCA TTCCACAAC
1051 ATCGTCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGATC GCTTTTCTTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTTCA TCCCTTTCGG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGC CATATTGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

```

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

```

```

51  AAGLIVLLFL TAGKKLFQDVK IPAISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNIDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVKVAEK
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

m738.pep	10	20	30	40	50	60
	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	MSAETTVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
m738.pep	70	80	90	100	110	120
	TAGKKLFQDVKIPAISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFQDVKIPAISFLLFAMAAFWWLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	130	140	150	160	170	180
	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
g738	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
m738.pep	190	200	210	220	230	240
	NLGHYLMWGILAAAYLNGQRKIPAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPEW					
g738	NLGHYLMWGILASAYLNGQRKIPAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPEW					
	190	200	210	220	230	240
m738.pep	250	260	270	280	290	300
	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNAILETFTGIRYETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	310	320	330	340	350	360
	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHNIDNLLSNLFTHSHNIVLQLLAEMG					
g738	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHTIHDNLFSTLFTSHNIIQLLAEMG					
	310	320	330	340	350	360
m738.pep	370	380	390	400	410	420
	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	ISGTLLVAATLLTGIAGLLKRSLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	430	440	450	460	470	480
	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
g738	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEAEATLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEAEATLKALKYRYPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQKGVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQKGVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPET					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738.seq
1  ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATTGTTTA
501 CAGCGGGCAA GCGGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGC CTTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACGCGCG TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGTCTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTCTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTTCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCGC CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738.pep
1  MPAETTVSGA HPAAKLPYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAA
51  AAGLIVLFLF TAGKKLFDVK IPPISFLLEF MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGOERIV TLFWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```

1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
 251 TILGIAAAVF LTALFQFSMN TILFTTGIR YETAVERVAN GGFTDLPRQI
 301 EWRKALAAEQ SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTHSHN
 351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAESDG IAFKKAANLG ILTASAAIFA
 451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVKVAEK
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
 601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQSPDFYHDAAGLIVLLFL					
m738	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
	70	80	90	100	110	120
a738.pep	TAGKKLFDVKIPPIISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
m738	TAGKKLFDVKIPPAISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a738.pep	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
m738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a738.pep	NLGHYLMWGILAAAYLNGQRKIPPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738	NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a738.pep	YFRSDKSNRRRTILGIAAAVF LTALFQFSMNTILEFTTGIRYETAVERVANGGFTDLPRQI					
m738	YFRSDKSNRRRTMLGIAAAVF LTALFQFSMNTILEFTTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a738.pep	EWRKALAAEQSAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTHSHNIVLQLLAEMG					
m738	EWNKALAAEQSAPIFGHGWN SFAQQTFLINAEQHNIDNLLSNLFTHSHNIVLQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a738.pep	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
m738	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
a738.pep	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTYRMVNAFSPATDDSAKTLNRK					
m738	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
	490	500	510	520	530	540
a738.pep	INELRYISANSPMLSFYADFSLVNFALEPY PETQTWAEATL KSLKYRPHSATYRIALYL					
m738	INELRYISANSPMLSFYADFSLVNFALEPY PETQTWAEATL KSLKYRPHSATYRIALYL					
	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738.pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDKAFAAAPGHPEA					
m738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDKAFAAAPGHPEA					
	550	560	570	580	590	600
a738.pep	KPCCKX					
m738	KPCCKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCTT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCAACCCGGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGGCCAA ACCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1  MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTESGSGLP
101 SPAAPKKNRVKPRPSDAARAADSLTGTGTQAENTLKETPV LPTNAPHPEP
151 RKETPEKQAQPKETPKKETPKENHTKPDTPKNTPAKPHKEILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCTT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCAACCCGGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAAGA
501 AAACCATACC AAACCGGACA CCCGAAAAA CAGCCGCCCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1  MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLP
101 SPAAPKKNRVKQPADTAQTDRQDDAGTQAENTLKETPV LPTNVPRPEP
151 RKETPEKQAQPKETPKENHTKPDTPKNTPPKPHKEILDKLF

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDGSGSLPSAAPKKNRVKQPADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
g739	ADSLTGTGTAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKTPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPKHEILDKLF					
g739	PKNTPAKPKHEILDNLFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1   ATGGCAAAAA AACC GAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATCAAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAACAA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAGAAA CACCCAAAGA
501 AAAAGAACG CCCAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCCATAA GAAATCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1   MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSLP
101 SPAAPKKNRV KQPADTAQT DRQPDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPHK EILDNLFX*

```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTE PQHTDSPRET					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDGSGSLPSAAPKKNRVKQPADTAQT					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDGSGSLPSAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDAGAQ AENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
m739	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

              190
a739.pep      PKNTPPKPKHKEILDNLFX
              |||||:|
m739          PKNTPPKPKHKEILDKLF
              180   190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATT
201 GAAACgtcaa ACCATGTTTC TGTTTATTCC GATTGTTTTC CTGGTTGTGT
251 ATTTGTTCCA CTATTTCCGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFEETIKHH LKQGFDLKRQ TMLFPIIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCCTT
51 GGCgACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 TTCGTCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KQHLINGII LACEATFLFK
51 FVLFDITIKHH LKQEFDLKRQ TMLFPIIIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

              10      20      30      40      50      60
m740.pep      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLQHLINGIILACEATFLFKFVLFDITIKHH
              |||||:|
g740          MSRNLLVRWLAVCLIPLATLAVFAANPPEDKPQHLINGIILACEATFLFKFVLEETIKHH
              10      20      30      40      50      60

              70      80      90
m740.pep      LKQEFDLKRQTMLLFPIIILLIVYLFHYFGAFX
              |||:|
g740          LKQGFDLKRQTMFLFPIIVLLVYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GGCgACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFDITIKHH LKQEFDLKRQ TMLFPIIIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

              10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLVLVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m740      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
          10      20      30      40      50      60

          70      80      90
a740.pep  LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m740      LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
          70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1  GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTG GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTGGGCG GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTGCG CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1  VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAETFK AGGKDNSLNT GKLNNDKISR
101 FDFVQKIEVD GQTITLASGE FQIYQDHS A VVALRIE KIN NPKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1  GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GCGGCGACAA GGTGCGGAAA AACTTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTAACCTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCGGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTGGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAGACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1  VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHKDKGL
51  QSLTLDQSVR KNEKLKLAAG GAEKTYGNGD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFTQ EQIQDSEHSG KMVAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYYTID FAAKQGNNGKI
 201 EHLKSPELNV DLAADIKPD GKRHAIVISGS VLYNQAEKGS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCSLT---	ALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQ			
g741	VNRTTFCCSLTAGPDSRLQRRGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEA				
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAQAQGAEKTY---	GNGDSLNTGKLKNDKVSRLFIRQIEVDGQLITLESGE			
g741	SIPQNGTLTSAQGAEKTFKAGGKDNSLNTGKLKNDKISRFDVQKIEVDGQTITLASGE				
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQTEQIQDSEHSKGMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGT				
g741	FQIYKQDHSAVVALRIEKINNFDKIDSLINQRSFLVSDLGGEHTAFNQLPDG-KAEYHGK				
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLTYYTIDFAAKQGNNGKIEHLKSPELNVDLAAADIKPDGKRHAIVISGSVLYN				
g741	AFSSDDADGKLTYYTIDFAAKQGHGKIEHLKTPQNVNELASAELKADEKSHAVILGDTRYG				
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKQX				
g741	GEEKGTYRLALFGDRAQEIAGSATVKIGEKVHEIGIADKQX				
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq

1	GTGAACCGAA	CTGCCTTCTG	CTGCCTTCTT	TTGACCGCCG	CCCTGATTCT
51	GACCGCCTGC	AGCAGCGGAG	GCGGCGGTGT	CGCCGCCGAC	ATCGGCGCGG
101	TGCTTGCCGA	TGCACTAACC	GCACCGCTCG	ACCATAAAGA	CAAAAGTTTG
151	CAGTCTTTGA	CGCTGGATCA	GTCCGTCAAG	AAAAACGAGA	AACTGAAGCT
201	GGCGGCACAA	GGTGCGGAAA	AAACTTATGG	AAACGGCGAC	AGCCTCAATA
251	CGGGCAAATT	GAAGAACGAC	AAGGTCAGCC	GCTTCGACTT	TATCCGTCAA
301	ATCGAAGTGG	ACGGGCAGCT	CATTACCTTG	GAGAGCGGAG	AGTTCCAAGT
351	GTACAAACAA	AGCCATTCCG	CCTTAACCGC	CCTTCAGACC	GAGCAAGTAC
401	AAGATTCGGA	GCATTCAGGG	AAGATGGTTG	CGAAACGCCA	GTTCAAGATC
451	GGCGATATAG	CGGGTGAACA	TACATCTTTT	GACAAGCTTC	CCGAAGGCGG
501	CAGGGCGACA	TATCGCGGGA	CGGCATTCCG	TTCAGACGAT	GCCAGTGGAA
551	AACTGACCTA	CACCATAGAT	TTCGCCGCCA	AGCAGGGACA	CGGCAAAATC
601	GAACATTTGA	AATCGCCAGA	ACTCAATGTT	GACCTGGCCG	CCTCCGATAT
651	CAAGCCGGAT	AAAAAACGCC	ATGCCGTCAT	CAGCGGTTCC	GTCCCTTTACA
701	ACCAAGCCGA	GAAAGGCAGT	TACTCTCTAG	GCATCTTTGG	CGGGCAAGCC
751	CAGGAAGTTG	CCGGCAGCGC	AGAAGTGAA	ACCGCAAACG	GCATACGCCA
801	TATCGGTCTT	CGCGCCAAGC	AGTAA		

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep

1	VNRTAFCCLS	LTAALILTAC	SSGGGGVAAD	IGAVLADALT	APLDHKDKSL
51	QSLTLDQSVR	KNEKLKLAQ	GAEKTYNGND	SLNTGKLKND	KVSRLFDFIRQ
101	IEVDGQLITL	ESGEFQYKQ	SHSALTALQT	EQVQDSEHS	KMVAKRQFRI
151	GDIAGEHTSF	DKLPEGGRAT	YRGTAFGSDD	ASGKLTYYTID	FAAKQGHGKI
201	EHLKSPELNV	DLAADIKPD	KKRHAIVISGS	VLYNQAEKGS	YSLGIFGGQA
251	QEVAGSAEVE	TANGIRHIGL	AAKQ*		

a741/m741 95.6% identity in 274 aa overlap

1207

a741.pep	10	20	30	40	50	60
	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	10	20	30	40	50	60
	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
a741.pep	70	80	90	100	110	120
	KNEKCLKLAAQGAEKTYGNGDGLNTGKLNKDKVSRFDIFRQIEVDGQLITLESGEFQVYKQ					
m741	70	80	90	100	110	120
	KNEKCLKLAAQGAEKTYGNGDGLNTGKLNKDKVSRFDIFRQIEVDGQLITLESGEFQVYKQ					
a741.pep	130	140	150	160	170	180
	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPPEGGRATYRGTAFGSD					
m741	130	140	150	160	170	180
	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPPEGGRATYRGTAFGSD					
a741.pep	190	200	210	220	230	240
	ASGKLTYYTIDFAAQQGHGKIEHLKSPELNVDLAASDIKPKKRHAVISGSVLYNQAEKGS					
m741	190	200	210	220	230	240
	AGGKLTYYTIDFAAQQNGKIEHLKSPELNVDLAADIKPKDKRHAVISGSVLYNQAEKGS					
a741.pep	250	260	270			
	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAAKQX					
m741	250	260	270			
	YSLGIFGGKAQEVAGSAEVKTNGIRHIGLAAKQX					

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATGGTTTACG	GCATTGCCGA	AGCCGATGCG	GGCGACAGCA	GTGTGCTTAC
51	TTTGGGCGGC	ATGTATCAGA	AGAGTAGGGA	GGTTCCTGAT	TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAT	CAGAAACTG	CCCCGTTTCA	TTCAACGCCT
151	GCCTGCAACC	GGCCTTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TTAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAC
251	ATGTGTTTGA	CAACGGTTGG	CAGCTCAATG	CCGAAGTGTC	TTATACCAAG
301	AATGAATCCG	ATGCCGAAGT	GGGGCAGTTT	TTTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG	TCGGGTGAGG	ATGCCGTAGG	CTTTTGTACT	GAAAAAACCG
401	AAGTCATCCC	GTTTCGAGCCG	AAAGATAAGG	CATTGGAGAA	ACTGAAAGCA
451	TATCGTGATG	AAACCGCCAA	GGAATACCGG	GAGCGCAAAG	ACGATTTTGT
501	TAAAAACCGT	TTTGATAATA	CTGCTTTCGA	ACAGTATCGC	AGCCGCCGTG
551	CCGCAGAACG	CAAAGCCGGT	TTTGACAAGT	GTATGAGTGA	CCCTTTCGCG
601	CTGGACTTTA	TCTGTCAAGG	TTCTTGGGGG	GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA	TTTGTGCGTA	AAGCCCTTGC	GAAGGAGGGC	ATCTTTAATA
701	ATGCGGCACA	ACGTTTTCCT	AACAGCCTGT	ATGACTCTTC	CTTTAATCCG
751	AAGGCTACCG	CCAACCGACG	ATACAGTTAT	ATGCCGTTGC	GGCATAACAA
801	AGACGACCGC	CAATGGGGAA	TAAACTTGA	CCTGACCGGC	ACATATGGGC
851	TGTTCGGGCG	GGAGCATGAT	TTCTTTGTGC	GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT	CGGAATATCT	AGAAATCTAC	GAACGCCGCT	ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGGACGG	CGATTGTGCG	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG	CGTACGATGA	AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT	GACGAATACA	GCGGCAGCCG	GACACCGGTA
1201	TATGTCGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAC
1251	CAATCCCAGC	GGCAGCCTG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCGG
1301	TTTGGAAAAC	CGTCAAAGTG	GCAGACGACC	ATGTTCCCTG	GCTGTATAAC
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTGCTGTA	CTGCCAGCAC
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTGCACTACA

1208

```

1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTCGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACCTC AGCAATTCA
2051 CACCCGTGCA CATATTCGGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGCGCG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACCTTAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

m742.pep

```

1 MVYGIAEADA GDSSVLTGG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
51 ACNRLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101 NESDAKVQGF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDKCMSDFPA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKDLTG TYGLFGREHD FFGVYAYGDE
301 KIRSEYLEIY ERRYVRPNT GATHGVYAGS CQEEPDGDL SFLVRGHKEP
351 DWQAYDEKGN RTVYAEERN AKKIKTEPKL DAEGKQVYYY DEYSRSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVKV ADDHVPALYN
451 YAKYLNTNKT HSLTASTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQDNDVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEDWKVFAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

a742.seq

```

1 ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCACAGCA GTGTGCTTAC
51 TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTATTTTGTC CTGTGAAAAT CAGAAACTG CCCCCTTCAG TTCAACGCCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTGAGTGCTG ACAATAACAA CCTTTTCTCA GGTTCCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAACATGC
351 GGCGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTCGA GCAGTACCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGGC
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTCGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 GTTCGGGCGG GGAGCATGAT TTCTTTGTCG GCTATGCCTA CGGCGATGAA
901 AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTACGGGGG
1001 AGCCGGACCG TGATTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

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a742.ppt

1	MVYGIAEADA	GDSSVLTGG	MYQKSREVPD	FSGIILSCEN	QKTAPFSSPT
51	ACNRPLQLPR	NTLGEADWSR	LSADKYNFVS	GFKHVFDNGW	QLNAEVSYTK
101	NESDAKVQGF	FLKNEHAAGL	SDEDAVNGFLT	EKNEVIPFEP	KDKALEKLKA
151	YRDETAKEYR	ERKDDFVKNR	FDNTAFEQYR	SRAEAERKAG	FDECMASFFA
201	LDFICQGSWG	DPGVDADKSE	FVDKALAKEG	IFNNAAQRF	NSLYDSSFNR
251	KATANRRYSY	MPLRHTKDDR	QWGIKLDLTD	TYGLFGREHD	FFVGAYGDE
301	KIRSEYLEIY	ERRHRVRPNT	GATHGVYAGS	CQGEPDGDL	SPLVRGHKEP
351	DWQAYDEKGN	RTVYAEERN	KKKIKTEPKL	DAEGKVQVY	DEYSGSRFTV
401	YVDVYELDEK	GNKIQETNPD	GTPAFTGFSG	TVPVWKTVKV	ADHDVPALYN
451	YAKYLNTAKT	HSLTAGTRFN	VTGRHLHLLG	LHYTRYETSP	TKDMPVRYGQ
501	PASDFQNTSS	IKADQDHYTA	KMGQHKLLTPY	AGITYDLTSP	QSIYGSYTKI
551	EKQDNDVDS	AKTVLPPLVG	TNYEVGWKG	FLQRLNASF	ALFYLEQKNR
601	TVVDFGYVPG	AGGKQGSFQT	VAKPIGVVS	RGAEFELSGE	LNEDWKVFFAG
651	YTYNKSGYKN	AAEVNAERLA	KNTGADPYNF	SNETPVHIFR	FGTSFHIPNT
701	GLTVGGYGS	QSGTSSLYNI	RQGGYGLIDG	FVRYELGKHA	KLSLIGTNLN
751	GRTYFENNYN	RTGRANFFYG	EPRTVSMKLD	WOF*	

a742/m742 98.5% identity in 783 aa overlap

	10	20	30	40	50	60
a742.pep	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILSCENQKTAPFSSSTPACNRPLQLPR					
m742	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILPCENQKTAPFSSSTPACNRPLQLPR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a742.pep	NTYLGEDWSRLSADKYNLFSGFKHVFNDNGWQLNAEVSYTKNESDAKVGQFFLKNEHAAGL					
m742	NTYLGEDWSRLSADKYNLFSGFKHVFNDNGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a742.pep	SDEDAVGFLTEKNEVIPFEPKD KALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
m742	SGEDAVGFLTEKNEVIPFEPKD KALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a742.pep	SRRAAERKAGFDECM SAPFALDFICQGSWGDGPVDADKSEFVDKALAKEGIENNAORF					

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|||||:|||||:|||||:|||||:|||||:|||||:
m742      SRRAAERKAGFDKCMSDPFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
          190      200      210      220      230      240

          250      260      270      280      290      300
a742.pep  NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKLDTGTGYGLFGREHDFVGYAYGDE
          250      260      270      280      290      300
m742      NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKLDTGTGTGLFGREHDFVGYAYGDE
          250      260      270      280      290      300

          310      320      330      340      350      360
a742.pep  KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEPDGDLSSPLVRGHKEPDWQAYDEKGN
          310      320      330      340      350      360
m742      KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEPDGDLSSPLVRGHKEPDWQAYDEKGN
          310      320      330      340      350      360

          370      380      390      400      410      420
a742.pep  RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQTNP
          370      380      390      400      410      420
m742      RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQTNP
          370      380      390      400      410      420

          430      440      450      460      470      480
a742.pep  GTPAFTGFSGTVPVWKTVKVADHDHVPALYNYAKYLNTNKTSLTAGTRFNVGTGRLHLLGG
          430      440      450      460      470      480
m742      GTPAFTGFSGTVPVWKTVKVADHDHVPALYNYAKYLNTNKTSLTAGTRFNVGTGRLHLLGG
          430      440      450      460      470      480

          490      500      510      520      530      540
a742.pep  LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTTPYAGITYDLTPQ
          490      500      510      520      530      540
m742      LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTTPYAGITYDLTPQ
          490      500      510      520      530      540

          550      560      570      580      590      600
a742.pep  QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRNLASFALFYLEQKNR
          550      560      570      580      590      600
m742      QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRNLASFALFYLEQKNR
          550      560      570      580      590      600

          610      620      630      640      650      660
a742.pep  TVVDFGYVPGAGGKQGSFQTVAKPIGKVSRGAEFELSGELNEDWKVFAGYTYNKSRYKN
          610      620      630      640      650      660
m742      TVVDFGYVPGAGGKQGSFQTVAKPIGKVSRGAEFELSGELNEDWKVFAGYTYNKSRYKN
          610      620      630      640      650      660

          670      680      690      700      710      720
a742.pep  AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          670      680      690      700      710      720
m742      AAEVNAERLAKNSADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          670      680      690      700      710      720

          730      740      750      760      770      780
a742.pep  RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          730      740      750      760      770      780
m742      RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          730      740      750      760      770      780

a742.pep  WQFX
          |||
m742      WQFX
```

a742/ p25184

sp|P25184|PUPA_PSEPU

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

>gi|94923|pir||S15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)
 pseudobactin uptake protein [*Pseudomonas putida*] Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADHDV-PALYNYAKYLNTNKTSLTAGTRFNVTLRLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y
 Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDLHLLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTYPAGITYDLTPQOSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRNLNASFALFYLEQKNRTVVDFGVYPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG
 Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMKRONLAESTNEVVPDSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + ++G + ELSGE+ W VF GY++ ++
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEGLVPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +
 Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGWEKLTGCGVWNSKSTLNFAFYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F
 Sbjct: 768 TSIMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTT CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGCGCAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGGGC GGTATTATGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRMSTATGM RIAGKDT PQS VSVITRSRLD DKAVHTLEEA
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTD LAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTT CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTG
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTATTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
1  MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
51  GKTEKTRSYT IDRMSTATGM RIAGKDPQS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTD LAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

```

              10      20      30      40      50      60
a743.pep  MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT
          |||
m743      MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT
              10      20      30      40      50      60

              70      80      90     100     110     120
a743.pep  IDRMSTATGMRIAGKDTQPQSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSSLQTRFL
          |||
m743      IDRMSTATGMRIAGKDTQPQSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSSLQTRFL
              70      80      90     100     110     120

              130     140     150     160     170     180
a743.pep  SRGFYIDQIGEDGITVNVAGRSGYTAKIDVSPSTD LAVYD HIEVVRGATGLTQSNSEPGG
          |||
m743      SRGFYIDQIGEDGMTVNVAGRSGYTAKIDVSPSTD LAVYD HIEVVRGATGLTQSNSEPGG
              130     140     150     160     170     180

a743.pep  TVNLIRKR
          |||
m743      TVNLIRKX

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g744.seq not found yet
g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
1  ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
51  CAGAAGAAGA GAAATAAAG ATTTATTTAA CCGAATATTT GTAAAGGAG
101 AATATTGGA TGAATTATGT GAACCAATA TTTCGTTTTT AATCGGAGAA
151 AAGGGAACGT GAAAGACAGC ATATGCTGTT TATTTAACATA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACGTGTTT AGATTTTACA
301 AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAGGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGTATCC GGAATTTGTA
451 CAAGCAATAA CTTTAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAAATTT GTTAAACTAG GTGAAGAGGA ATCCCAACAA ATAACCTTTA
551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTATTATGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAGAGG TCTTGCTAAC GCCATATGGA TGTAAATAAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAT ACCCAACTTC
851 AAGATAATTC AGTATTTTTA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGTAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTAGAAA AAGGCAACTC ATGGGATTAT TATTTCCCT
1001 GGAATGCTCC TAATTACAT GATGAGTATA AAAATTTAAC TTCATTATT
1051 AGCTTCCTAA GAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTCCTG AAATTTTTTG AATTTTAAA CGGGAAGAT AGATTTAAAT

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAAAC TGAAACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

```

m744.pep
  1 MKPLKTLFEG FVDAANYRRR ENKDLFNRIE VKGEYLDLCE EPNISFLIGE
  51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
 101 SIWKVILYLL ISNQIKCKEN GILSSIENKF KALDEAINEY YYGAFDPEIV
 151 QAITLIENSK EAAEMIFGKF VKLGEESQO ITFTESKFOA NLGFIERKFK
 201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
 251 PSIKDSKGRM RVVLLIRPDI FDSLGLQONN TKLQDNSVFL DWRTDYKSYR
 301 SSKIFGVFDH LLRTQQEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
 351 SFRLKSYRPP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
 401 GEIKDHLLEY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
 451 TSVEIPKFMS TANEFLQFLF DLNVIAYLDN PEDETKPIYH WCFKDRNYAN
 501 ISPKIKTETE YLIFSGLSKA LDVGTPEKKN Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

```

m745.seq
  1 ATGTTTTGGC AACTGACCGT TGTTCAGTA ACCGCCGTCA TTGCACTGGG
  51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAGGCG ACATTAGATG
 101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
 151 ATTCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
 201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
 251 GAGGCGATTT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TCGGTGCGCA
 301 ATCAACTCGG GAGTATTGGA TGAGGATTTG TTTAAACGGC TGCATTGCAC
 351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
 401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTTT
 451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGTG GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

```

m745.pep
  1 MFWQLTVVSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
  51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
 101 INSGVLDEDL FKRLHCTNFI KLNWVASPLV MKIREEERKD TIFRELEILV
 151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

```

g746.seq
  1 ATGTCGGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
  51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
 101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
 151 CCCGCACCGC AGGCCGGCGA AACCGGCGCA ACGGAAAGCC AAACGGCAAA
 201 CACGGCACAA ACCCTGCCT TGAATCCGC CGCCGAAAAAC GGGGAAACCG
 251 CGCCGCACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
 301 GACAGCGAAA TCAGCGAGCC TGAAAACGTA GGCGCCGCCG TGGTGCTGAT
 351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGGA GAATCCGAGA
 401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCGAAGCA GGCAAAACAA
 451 CGCGCTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
 501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
 551 GCACTGCCGA AGCCAAGCCC AAAGCCAAG AAACCAAAAC CGCCGAAAAA
 601 GTTGCCGACA AACCGAAAAC TGCTGCCGAA AAAACCAAC CGGATACGGC
 651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
 701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

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1214

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751 GCGCAAAAAA CCGACAAAGC GGACAAAACC AAAACCGCCG AGAAGGAAAA
801 ATCCGGCAAG GCGGGCAAAA AAGCCGCCAT TCAGGCAGGT TATGCCGAAA
851 AAGAACGCCG CTTGAGCCTC CAGCGCAAAA TGAAGCGCGC GGTATCGAT
901 TCGACCATCA CCGAAATCAT GACCGACAAC GGCAAGTTT ACCGCGTCAA
951 ATCAAGCAAC TATAAAAACG CAAGGGATGC CGAACGCGAT TTGAACAAAC
1001 TCGCGGTGCA CGGCATCGCC GGCCAGGTAA CGAATGAATA G

```

This corresponds to the amino acid sequence <SEQ ID 2552; ORF 746.ng>:

```

g746.pep
1  MSENKQNEVL TGYEQLKRRN RRRLVTASSL VAASCILLAA ALSSDPADSN
51  PAPQAGETGA TESQTANTAQ TPALKSAAEN GETAADKPQD LAGEDKPSAA
101 DSEISEPENV GAPLVLINDR LEDSNIKGLE ESEKLQQAET AKTEPKQAKQ
151 RAAEKVSATA DSTDTVAVEK PKRTAEPKPQ KAERTAEAKP KAKETKTAEK
201 VADKPKTAEE KTKPDTAKSD SAVKEAKKAD KAEGKKTAEK DRSDGKKHET
251 AQKTDKADKT KTAEEKESGK AGKKAIIQAG YAEKERALS L QRMKAAGID
301 STITEIMTDN GKVYRVKSSN YKNARDAERD LNKLRVHGIA GQVTNE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2553>:

```

m746.seq
1  ATGTCGGAAC ACAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51  ACGGGCGCAAC CGCCGCGGCC TCGTAACGGC AAGTTGCCTG GTTGCCGCGCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCCGGCGGAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCGC CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCGGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGAGCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGA AAAACCG AAACGCCTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAA GCGCAAGAAA
551 CCAAAACCGC CGAAAAGTT GCCGACAAAC CGAAAACCTG CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
651 AGCCGACAA GCTGAAAGCA AAAAACAGC CGAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAGCGGA CAAGACCAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCCGCCATT AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
851 GTATCGATT CACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAA CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATT
951 GAACAAATTG CGCGTACAG GTATCGCCG TCAGGTAACG AATGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2554; ORF 746>:

```

m746.pep
1  MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINERL EDSNIKGLEA SEKLQQAETA KTAPKQAKR AAEKVPTAD
151 STDTVAVEKP KRTAETKPK AERTAKAPK AKETKTAEKV ADRPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADTK
251 TAEKEKSGK AAIQAGYAEK ERALS LQRM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

```

m746/g746      89.9% identity in 346 aa overlap

          10      20      30      40      50
m746.pep  MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQT----AGETSG
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
g746       MSENKQNEVL TGYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGA
          10      20      30      40      50      60

          60      70      80      90     100     109
m746.pep  VENKAAGAAQT PALKSAA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER
          :|:::|:::|||||:::|||||:::|||||:::|||||:::|||||:::
g746       TESQTANTAQT PALKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR
          70      80      90     100     110     120

```

	110	120	130	140	150	160	169
m746.pep	LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETRPQ						
g746	LEDSNIKGLEASEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPQ						
	130	140	150	160	170	180	
	170	180	190	200	210	220	229
m746.pep	KAERTAKAKPKAKETKTKAEKVADKPKTAAEKT KPD TAKSDSAVKEAKKADKAESKKTAEK						
g746	KAERTAEAKPKAKETKTKAEKVADKPKTAAEKT KPD TAKSDSAVKEAKKADKAEGKKTAEK						
	190	200	210	220	230	240	
	230	240	250	260	270	280	
m746.pep	DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALS LQRKMKKAAGID						
g746	DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALS LQRKMKKAAGID						
	250	260	270	280	290	300	
	290	300	310	320	330		
m746.pep	STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX						
g746	STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX						
	310	320	330	340			

a746.seq

a746.pgp

a746.pep 10 20 30 40 50 60
 MSENKQNEVLSGGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
 |||||
 m746 MSENKQNEVLSGGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
 10 20 30 40 50 60

1216

```

          70      80      90      100     110     120
a746.pep  AAGAAQTPLKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA
          |||||
m746      AAGAAQTPLKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA
          70      80      90      100     110     120

          130     140     150     160     170     180
a746.pep  SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK
          |||||
m746      SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK
          130     140     150     160     170     180

          190     200     210     220     230     240
a746.pep  AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          |||||
m746      AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          190     200     210     220     230     240

          250     260     270     280     290     300
a746.pep  QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY
          |||||
m746      QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY
          250     260     270     280     290     300

          310     320     330
a746.pep  RVKSSNYKNARDAERDLNKLVRVHGIAGQVTNEX
          |||||
m746      RVKSSNYKNARDAERDLNKLVRVHGIAGQVTNEX
          310     320     330

```

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGACG  GTGACAAAAC CAAATGGGC  CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

```

m747.pep
1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HHTIYKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGACG  GCGACAAAAC CAAATGGGC  CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

```

a747.pep
1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```

a747.pep      10      20      30      40      50      60
               LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLVGKQLTDSVGLFDPYYR
               |||||
m747          10      20      30      40      50      60
               LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGWSVGIGLVGKQLTDSVGLFDPYYR
               |||||

a747.pep      70      80      90      100
               HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
               |||||
m747          70      80      90      100
               HKTIYKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
               |||||

```

a747/m80195

gi|150271 (M80195) outer membrane protein [Neisseria meningitidis] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLVGKQLTDSVGLFDPYYR 60

+ PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+

Sbjct: 174 INPWSEVKFDLNSRYKLNTGVNLLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95

+T + E + GD + ++ EYG RV F

Sbjct: 234 QRTYKESGEFSVTTKSGDVSILTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

```

1 ATGAGTCAAA ACCAACC CGC ACAACCGACC AAACGCAATC TGTTCAAAAC
51 CGCCCTTGCC GTCGGCGCAA TCGGCGCAAT CGGAGGTTAT TTCGGCGGCA
101 AAAAAACAGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151 CAAGCCTATC CCTGTACGG CGAACATCAG GCAGGTATCG TTACGCCCGG
201 GCAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGCGG GAGAATACCA AGACGGCGAC GACAAACTCC CGTCAGCCGG
351 CAGCGGCATT TTGGGTAAAG CTTCAACCC CGACGGATTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGGACGGCG ATTTGAGCCT GCAAACTGCG GCCTTCACCC
551 CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAAAACA CACCGCCCAA
601 ACCGCCGTCA TCCGTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
701 ACCCAAGGT TTCCGATCCC AAAACCGCCG ACGAGGTTTT ATGGACGGGC
751 GTGGCCGCCA ACAGCTTCGA CGAACCGGAG TGGCGAAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCGCTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGAAAAATA CAGCGGGGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTC CCAAAGACCC
951 CGAGGGTGAT ATCAGCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCTCAAA AAACACTGCC TCTTCGCGCG CGCCTACAGC
1051 TATTCTCGCG GACCCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAATC TTGCCGACGG TTTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTCTTCG TCTTGCCCGG CGTGGGAAAA GCGGATTCT TGGGACAAGG
1251 GCTGCCGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

```

1 MSQNQAQPT KRNLFKTALA VGAIGAIGGY FGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPROAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGGYQDGD DKLPASAGSI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KTVHLQEMRD FPNKLOKSW CDGDLSQLIC AFTPETCQTA LRDIKHATAQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRFEFEW DRTPLEQETD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHMRL ANPRDPEFLK KHCLFRFRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLLNGEPL EEYISPFGGG

```


401 YFFVLPGVGK GGFLGQGLPG V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

```
m748.seq
1  ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51  CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAG CTTCAACCC CGACGGGTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATT CATTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGCGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAAAC CACCGTCCAA
601 ACCGCCGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCGGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTACGGGAC GGCACGGGCA
701 ACCCCAAAGT TTCCGATCCC AAAACTCGCG ACGAGGTTTT GTGGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCGAAATA CAGCGGTGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
951 CGAGGGTGAT ATCAGCCCCA AAGACAGCCA TATACGCTCG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACCGCC TCTTCGCGCG CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCT GGCTGGTGT
1101 CGTCTGCTAT CAGGCAAACC TTGCGGACGG ATTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTTT CGGCGGCGGC
1201 TATTTCTTCG TCTTGCCCGG CGTGGA AAAA GCGGCTTTT TGGGCAAGG
1251 GCTGCTGGGC GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

```
m748.pep
1  MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGGEYQDGD DKLPPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLQLQIC AFTPETQQA LRDIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEOTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRFRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGEIF VQNLNGEPL EYISPFGGG
401 YFFVLPGVGK GGFLGQGLLG V*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

```
m748/g748 95.0% identity in 421 aa overlap

      10      20      30      40      50      60
m748.pep MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSPQAYPCYGEHQ
g748      MSQNPQAQPTKRNLFKTALAVGAIGAIGGYFGKKQGETAERTAESQHSPQAYPCYGEHQ
      10      20      30      40      50      60

      70      80      90     100     110     120
m748.pep AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGD LPPAGSGI
g748      AGIVTPRQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGD LPSAGSGI
      70      80      90     100     110     120

      130     140     150     160     170     180
m748.pep LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC
g748      LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKTVHLQEMRDFPNDKLQKSWCDGDLQLQIC
      130     140     150     160     170     180

      190     200     210     220     230     240
m748.pep AFTPETQQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
```

	190	200	210	220	230	240
g748	ATPETCQTALRDIKHTAQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748.pep	KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA					
g748	KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRRFVEFWDRTPLQEQTDFGRRKYSGA					
m748.pep	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRAYSYSRGLASSGQ					
g748	PMDGKKEADQPDFAKDPEGDITPKDSHMLANPRDPEFLKKHCLFRAYSYSRGPASSGQ					
m748.pep	LDVGLVFVCYQANLADGFIQVQNLLNGEPL E E Y I S P F G G G Y F F V L P G V E K G G F L G Q G L L G					
g748	LDVGLVFVCYQANLADGFIQVQNLLNGEPL E E Y I S P F G G G Y F F V L P G V G K G G F L G Q G L P G					
m748.pep	VX					
q748	VX					

```

a748.seq
1  ATGAGCAAAA ACCAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51  CGCGATCGCA GCTGGAGCAG TCGGCGCAAT CGGAGGTTAT TCGGCGGCCA
101 AAAAACGGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151 CAAGCTCATC TCTGTTACGG CGACATCATG CAGGCGATCG TTAAGCCGCA
201 CGAGGCGTTT CCGATTATGT GCGGCTTCGA CGTAAGCCGG CCAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG TCGAATACCA ACCTCGAGCC GACAAACTTC CGCCAGCGCG
351 CAGCGGCATT GTGGCAAAAG CGCTCAACGC CAGCGGGTTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATT ATTTCTAGGA AATCGCGCAC TTCTCCAAAG ATTAAGCTGCA
501 AAAAACCTGG TCGCAGCGCG ATTTGAGCCT GCAAACTCTG GTCCTCAACC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601 ACCCGCGTTA TCGCGTGGAG TATCAGCGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGCAT GCGCGCGCA ACCTGTTGGG TCTCCGCGAC GGCACGGGCA
701 ACCCCAAAGT TTCGACCCC AAAACTGCCG ACGAGGTTTT GTGGACGGGG
751 GTGGCGGCCA ACAGCTCTGA CGACCTCGAG TGGGCGAAAA ACGCGAGTAA
801 TCAGGCAGTC GCCTTATCC GCAATTTTGT TGAATTTTGG CAGCGACGCG
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGCAAATA CAGCGGCGCG
901 CGGATGGAGC GCAA AAAAGA AGACGACCAA CCGAGTTTGT CCAAGAACCC
951 CGAGGGGAAT ACCACGCCCA AAGCAGACCA TCATAGCTCT GCGAATCCGC
1001 GCGATCCCGA GTTCTTAA AACCACCGCC TCTTCCGCGC CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATATCT GGCTGGTGTG
1101 CGTCTGCTAT CAGGCAAAAC TTGCCGACGG ATTATCTTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCCCT CGGCGGCGGC
1201 TATTTCTTCG TCTTCCCGG CGTGGAAAAA GCGCGCTTTT TGGGCGAAGG
1251 GCTGCTGGGG GTATAA

```

```

a748.pep
1 MSKNQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKRGETA ERTAESQHSF
51 QAYPCYGEHQ AKIVTPQAAE SIMCAFDVTA QSAQLENLF RDLTRIEFL
101 TQGGEGYDGD DKLPPAGSGI LGKAFNPDL TVTVVGSSSL FTDRFGLKDK
151 KPIHLQEMRD FSNDKLQGSW CDGDLSLQIC AFTPETCQAA LRDIKHTVQ
201 TAVIRWSIDG WQKPSEGM AARNRLGFRD GTGNPKVSTG KTADEVLTSG
251 VAANSLDEPE WAKNGSYQAV RLRIHFVEFV DRTLQEQSDT IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGN TTPKDSHRL ANPRDPEFLK KHRLFRAYS
351 YSRGLASSGQ LGGVLVFCVY QANLADGFIF VQNLNNGEPL EEYISPFGGG
401 YFFVLPGVEK LDVPLGGLLG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

	10	20	30	40	50	60
a748 .pep	MSKNQPAQPTTRRTLFKTAIAAGAVGAIGGYLGGKKRGETAERTAESQHSFQAYPCYGEHQ					
m748	MSKKQPAQPTTRRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSFQAYPCYGEHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a748 .pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLRTARIEFLTQGGEYQDGGDKLPPAGSGI					
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLRTARIEFLTQGGEYQDGGDKLPPAGSGI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a748 .pep	LGKAENPDGLT VTVGVGSSLF DGRFGLKDKKPIHLQEMRDFSNDKLOKSWCDGDL SLQIC					
m748	LGKAENPDGLT VTVGVGSSLF DGRFGLKDKKPIHLQEMRDFSNDKLOKSWCDGDL SLQIC					
	130	140	150	160	170	180
	190	200	210	220	230	240
a748 .pep	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a748 .pep	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQT DIFGRRKYSGA					
m748	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQT DIFGRRKYSGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
a748 .pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
m748	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a748 .pep	LDVGLVFVCYQANLADGFI FVQNLNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
m748	LDVGLVFVCYQANLADGFI FVQNLNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
	370	380	390	400	410	420
a748 .pep	VX					
m748	VX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

```

1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTGGGTTT
51  GACCGCGTGC CAGCCGCCGG AGCGGAGAAA AGCCGCGCCG GCCCGTCCG
101 GTGAGACCCA ATCCGCCAAC GAAGCGGTT CGGTCGGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GAATCTGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AGGGCGTGAT GGTGGTGGAC GAACGCGAAA ATATCGCCCC GGGGCTTTCC
301 GACAAAATGA CCGTAaccct GCTGCCGGGC GAATACGAAA TGACCTGCGG
351 CCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAGCCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGCCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG CGGCGAAAAC
501 CAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTGCG CGCCACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATCGGTGTG AAGACGACTT
651 CAAAGACGGT CGGAAAGATG CCGGGTTTAC CGGCTTCCAC CGTATCGAAC
701 ACGCCCTTTG GGTGGAAAAA GACGTATCCG GCGTGAAGGA AACC GCGGCC
751 AAACCTGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATGGC

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801	GttccctCGG	GGCAAAGTGG	TCGGCGGCGC	GTCCGAAC TG	ATTGAAGAAG
851	CGGGCGGCGAG	TAAATACGAC	GGCGAAGAAG	ACCgttaACG	CCACCCGGAT
901	TTGAGCGCAT	TCCAAGCTAA	TCGGCGACGA	TC TAAAAAAA	TCGTGCGATT
951	GTTCGCTGCT	TGTATTGAGG	CCAAATCAAC	AGCCTTGTTG	GAAAAAACCG
1001	ATACCAACTT	CAACACGGTG	AACGAAATTA	TGGCGAAATT	CCGACACAAA
1051	GACGGTTTTG	AAACCTACGA	CAAGCTGAGC	GAAGCCGACC	CGAAAGCATT
1101	ACAGGCTCCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGGTT	GAAATAAA			

g749.pap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

1	ATGAGAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCGCCCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAA	GAGGCGGGT	CGGTGAGTAT	CGCCGCTCAAC
151	GCAATAGCCT	CGCAACCGAT	GGAACTGACC	GTGCGCAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGGTAT	GGTGGTGGAC	GAGCGCGAAA	ACATCTGCCC	CGGAGTTTCC
301	GACAAATAGA	CCGTCAACCT	GTGGCCGGGG	GAATACGAAA	TGACTTGGGG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACAACCG	CAACGACGCG	GATTTGGAAA	AACGTGCCCA	ACCCGTCGCC
451	GACTATAAAG	CTACGTTTCA	AGGCCAGGTT	AAAGAGCTGG	TGGCGAAAAA
501	CAAAACTTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGCGCAAAAT
551	CCCTGTTTGC	CGACACCCGC	GTPCATTACG	AACCGATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCGGTCTAG	GATGCGCGTG	AAGACGACTT
651	CAACAGACGC	GCGAAAGATG	CCGGAATTAC	CGGCTTTCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCGG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGTATG	CCGATGTGCA	AGCCCTGCAA	AAAGAAATCG	ACGCAATTGGC
801	TTTCTCTCCG	GCGAAGTGTG	TGCGGCGCGC	GTCGGAATCG	ATTGAAGAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAAG	ATCCGTACAG	CCACACCGAT
901	TTGAGCGCAT	TCCAAGCCAG	TGTGGACGGA	TCTAAAAAAA	TCGTGCAATT
951	TTTCGCTCCG	GTCATCGAGG	CCAAAAACA	AGCCTTGTAT	GAAAAAATCCG
1001	ATACCAACTT	CAACAGGTT	ACGAAATTC	TGGCGGAATA	CCCGACTAAA
1051	GACGGTTTGT	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAAGCGTT
1101	ACAGGCGCTT	ATAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTC	GAAATAA			

m749.pap

1	MRKFNLTLALS	VMLALGLTAC	QPPEAEKARP	AASGEAQ TAN	EGGSVSI AVN
51	DNACEPTMETS	VPSGQGVFNI	KNNSSGRKLEW	ELIKRGMVVD	ERENIAPGLS
101	DKMTVTLLPG	EYEMTCGLLT	PNRGLKV LVD	SGFKDTANEA	DLEKLSQPLA
151	DYKAYVQGEV	KELVAKTKFD	TEAVKAGDIE	KAKSLFADTR	VHYERIEPIA
201	ELFSELDPEI	DAREDDFKTF	AKDAAGTGFH	RIEYALWVEK	DVSGVKEIAH
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	TEEVAGSKIS	GDSDYSHTD
301	LDGFQANVDG	SKKI VDLFRP	LIEAKNNLAK	EKTD TNFQKV	NEILAKYR TK
351	DGFETYDKLG	EADRALQAS	INALAEDLAQ	LRGLGLGK*	

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

m749.pep MRKFNLTALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSIIVNDNACEPMELT
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 g749 MRKFNLTALSVMLALGLTACQPPEAEKAAPASGETQSANEGGSVGIIVNDNACEPMNLT
 10 20 30 40 50 60

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	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNSGRKLWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRVHYERIEPIAELEFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

1	ATGAGAAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCCGCTGC	CAGCCGCCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGCGGGTT	CGGTCAGTAT	CGCCGTCAAC
151	GACAAATGCT	GCGAACCAGT	GGAAGTACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCACCCCT	GTTGCCGGGC	GAATACGAAA	TGACTTGCGG
351	TCITTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCCG	CAACGAAGCG	GATTGGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTC	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATCGCGGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTCTA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCGC	GTCCGAAGTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTCGATTT
951	GTTCCGTCGG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTTG	GAATAAACCG
1001	ATACCAACTT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTGG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAATAAA			

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

1	MRKFNLTALS	VMLALGLTAC	QPPEAERAAP	AASGEAQTAN	EGGSVSIAVN
51	DNACEFMELT	VPSGQVVFNI	KNNSGRKLWE	EILKGVVVDD	ERENIAPGLS
101	DKMTVTLLPG	EYEMTCGLLT	NPRGKLVVTD	SGFKDTANEA	DLEKLSQPLA
151	DYKAYVQGEV	KELVAKTKTF	TEAVKAGDIE	KAKSLFADTR	VHYERIEPIA
201	ELFSELDPIV	DAREDDFKDG	AKDAGFTGFH	RIEYALWVEK	DVSGVKEIAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	IEEVAGSKIS	GEEDRYSHTD

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301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNL	TALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT			
m749	MRKFNL	TALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT			
	10	20	30	40	50	60
	70	80	90	100	110	120
a749.pep	VPSGQVVFN	IKNNSGRKLEWEILKGMVVD	ERENIAPGLSDKMTVTLLPGEYEMTCGLLT			
m749	VPSGQVVFN	IKNNSGRKLEWEILKGMVVD	ERENIAPGLSDKMTVTLLPGEYEMTCGLLT			
	70	80	90	100	110	120
	130	140	150	160	170	180
a749.pep	NPRGKLVVT	DSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFT	EAVKAGDIE			
m749	NPRGKLVVT	DSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFT	EAVKAGDIE			
	130	140	150	160	170	180
	190	200	210	220	230	240
a749.pep	KAKSLFADTRVHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
m749	KAKSLFADTRVHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
	190	200	210	220	230	240
	250	260	270	280	290	300
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVG	GASELIEEVAGSKISGEEDRYSH	TD			
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVG	GASELIEEVAGSKISGEEDRYSH	TD			
	250	260	270	280	290	300
	310	320	330	340	350	360
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTD	TNFKQVNEILAKYRTK	DGFETYDKLG			
m749	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTD	TNFKQVNEILAKYRTK	DGFETYDKLG			
	310	320	330	340	350	360
	370	380	389			
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq
 1 GTGAAACCGC GTTTTATTG GGCAGcctGC GCCGTCCTGC CGGCCGCCCTG
 51 TTCGCCCGAA CCTGCCGCCG AAAAACTGT ATccgCCGCA TCCCAAGCCG
 101 CATCCACACC TGTCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC
 151 GTTGTGCCGA AGAATCCCGA ACgcgtcgcc gtgtAcgaCt ggCGGGCGTt
 201 ggaTACGCTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG
 251 TGCGCGTGGA CTATTGCGAG CCTGCATTG ACAAGGCGGC AACGGTGGGG
 301 ACGCTGTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAATT
 351 TGTCATTACC GCGGGGCCGG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
 401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
 451 GCGGAGAAGC AGATGGAGAC CCTGTCGCGG ATTTTCGGTA AGGAAGCGCG
 501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCGCC CAAAAGCGCG
 551 AAGCCGCCAA AGGCAAGGA CGCGGGCTGG TGCTGTCCGT TACAGGCAAC
 601 AAGGTGTCCG CCTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
 651 CGACATCGGC CTGCCGCCCG TGGACGAATC TTTACGCAAC GAAGGGCACG
 701 GGCAGCCCGT TTCCTTCGAA TACATCAAAG AGAAAAACCC CGGCTGGATT
 751 TTCATCATCG ACCGCACCGC CGCATCGGG CAGGAAGGGC CGGCTGCCGT

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801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGGAAGCGCA
 851 AGCAAAATCAT CGTCATGCCT GCCGCGAACT ACATTGTGCG GGGCGGCGCG
 901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAAGGC
 951 AGAACCCGTT GCGGCGCAGT AG

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

g750.pep

1 VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
 51 VVFKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLQ PAFDKAATVG
 101 TLFEPDCESL HRHNPQFVIT GGPGAAYEQ LAKNATTIDL TVDNGNIRTS
 151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKGKG RGLVLSVTGN
 201 KVSFAFTQSR LASWIHGDIQ LPPVDESIRN EGHGQPVSE YIKEKNPGWI
 251 FIIDRTAAIG QEGFAAVEVL DNALVCGTNA WKRKQIIVMP AANYIVAGGA
 301 RQLIQAAEQL KAAFEKAEPV AAQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

m750.seq

1 GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
 51 TTCGCCGGA CTTGCCGCCG AAAAACTGT ATCCGCCGCA TCCGCATCTG
 101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
 151 AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTGG ATACGCTGAC
 201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGTG CGCGTGGATT
 251 ATTTGACGCC TGCAATTTGAC AAGCGGCAA CGGTGGGAC GCTGTTGAG
 301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
 351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCACCA
 401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAAGCG CGAAAAGCAG
 451 ATGGAGACCT TGGCGCGGAT TTTGCGCAAG GAAGCGCGCG CGGCGGAATT
 501 GAAGGCGCAG ATTGACGCGC TGTTCGCCCA AACGCGCGAA GCCGCCAAG
 551 GCAAAGGACG CGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCGCC
 601 TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
 651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
 701 CCTTCGAATA CATCAAGAG AAAAAACCCG ATTGGATTTT CATCATCGAC
 751 CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGCTGTGCG AAGTATTGGA
 801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
 851 TCATGCTGCG CGGCAACTAC ATTGTCGCGG GCGGCGCGCG GCAGTTGATT
 901 CAGGCGGCGG AGCAGTTGAA GCGGCGGTTT AAAAAGGCAG AACCCGTTGC
 951 GCGGGGAAAA AAGTAG

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

m750.pep

1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
 51 NPERVAVDW AALDTLTELQ VNVGATTAPV RVDYLQPAFD KAATVGTLFE
 101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
 151 METLARIFGK EARAELKAO IDALFAQTR AAKGKGRGLV LSVTGNKQSA
 201 FGTQSRSLASW IHGDIQLFPV DESLRNEGHG QPVSEFYIKE KNPWFIFIID
 251 RTAAIGQEGP AAVEVLNLA VRGTNAWKRK QIIVMPAANY IVAGGARQLI
 301 QAEEQLKAAF KKAEPVAAGK K*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

	10	20	30	40	50
m750.pep	VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASA-----ATLTVPPTARGDAVVPKNPERVA				
g750	VKPRFYWAACAVLPAACSPEPAAEKTVSAAASQAASTPVATLTVPPTARGDAVVPKNPERVA				
	10	20	30	40	50
	60	70	80	90	100
m750.pep	VYDWAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLPDYALHRYNPQLVIT				
g750	VYDWAALDTLTEPGNVGATTAPVRVDYLQPAFDKAATVGTLPDCESLHRHNPQFVIT				
	70	80	90	100	110
	120	130	140	150	160
m750.pep	GGPGAAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFA				

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g750      GGPGAEEAYEQLAKNATTIDLTVDNGNIRTSGEKOMETLSRIFGKEARVAELNAQIDALFA
           130      140      150      160      170      180

           180      190      200      210      220      230
m750.pep  QTREAAKGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      QKREAAKGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF
           190      200      210      220      230      240

           240      250      260      270      280      290
m750.pep  YIKEKNPFDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      YIKEKNPGWIFIIDRTAAIGQEGPAAVEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGA
           250      260      270      280      290      300

           300      310      320
m750.pep  RQLIQAAEQLKAAFKKAEFPVAAQKX
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      RQLIQAAEQLKAAFEKAEFPVAAQX
           310      320

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

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2750..seq
1      GTGAAAACCGC GTTTTTATTG GGCAGCGCTGC GCCGTCCTGC TGACCGCGCTG
51     TTCGCCCGGAA CTTGCCGCGC AAAAAAAGTGT ATCCGCCGCA TCCGCATCTG
101    CCGCCACACT   GACCGTGCCG ACCCGCGGGG GCGATGCCGT TGTGCCGAAG
151    AATCCCGAAG   GCGTCGCCCT GTACGCACTG GCGGCGCTTG ATACCGCTGAC
201    CGAAATGGGT   GTGAATGTGG GCGCAACCCAC CGCGCGGGTG CGCGTGGAAT
251    ATTTGCAGCC   TGCATTTGAC AAGCGCGCAA CGTGGGGGAC GCTGTTCCGAG
301    CCGGATTACG   AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351    CGGGCCGGGG   CGGGAAGCGT ATGAACAGTT GCGCAAAAAA CGCACCCACA
401    TAGATCTGAC   GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451    ATGGAGACCT   TGGCGCGGAT TTTCGGCAAG GAAGCGCGGAG CGGCGCGAAT
501    GGAAGGCGCAG   ATTGACGCGC TTTTCGCCCA AACGCGCGGA GCGCCCAAAG
551    GCAAAGGACG   CGGGCTGGTG CTGTGCGGTA CGGGCAACAA GGTGTCGCCC
601    TTCGCCACGC   AGTCGCGGTT GGCACAATTGG ATACACGGCG ACATCGGCCCT
651    ACCGCTGTGA   AGCAATCTTT TACGCAAGTGA GGGCGACCGG CAGCCTGTGT
701    CTTTCGAATA   CATCAAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
751    CGTACCGCGC   CCATCGGGCA GGAAGGGCCG GCGGCTGTGC AAGTATTGGA
801    TAACGCGCTG   GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAATCATCTG
851    TCATGCTGCG   CGCGAAGTAC ATTGTCGCGG GCGGCTCGCG GCAGTTGATT
901    CAGCGCGGCG   AGCAAGTTGA GGAGGCGGTT GAAAAGGCAG AACCCTGTGC
951    GCGCGGGAAA   GAGTAG

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This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

a750.pep

1	VKPRFYWAAC	AVLLTACSP	E	PAAEKTVSAA	SASAATLTVP	TARGDAVVPK
51	NPERRAVYDW	AALDTITELG	E	VNVGATTAPV	RVLYLQPAFD	KAAVTGLTFE
101	PDYEALHRYN	PQLVYTGPGP	E	AEAYEQLAKN	ATTIDLTVDN	GNIRTSGEKQ
151	METLARIFFGK	EARGAELKAQ	E	IDALFAQTRE	AAKGKGRGLV	LSVTGNKVS
201	FGTQSRSLASW	THRGDGLPPV	E	DESLRNHGNG	QPVSFGEYIKE	KNPDWIFIID
251	RTAAITQGEQF	EAEVFDLNAL	E	VRGTNAWKRK	QIIVMPAANY	IVAGGSRQLI
301	QAEEQLKEAF	EAKPEPVAAGK	E	E*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

a750/m750 98.8% identity in 321 aa overlap

	10	20	30	40	50	60
a750.pep	VKPRFYWAACAVLLTACSPEPAAEKTVSAASASAATLTVP	TARGDAVVPKNPERVA	VYDW			
m750	VKPRFYWAACAVLLTACSPEPAAEKTVSAASASAATLTVP	TARGDAVVPKNPERVA	VYDW			
	10	20	30	40	50	60
	70	80	90	100	110	120
a750.pep	AALDTLTELGVNVGATTAPVRVDYLQPAFDKAA	TGTLFEPDYEALHRYNPQLVITGGPG				
m750	AALDTLTELGVNVGATTAPVRVDYLQPAFDKAA	TGTLFEPDYEALHRYNPQLVITGGPG				

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	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVSFAFGTQSRSLASWIHGDIGLPPVDES LRNEGHGQPVSFEYIKE					
m750	AAKGKGRGLVLSVTGNKVSFAFGTQSRSLASWIHGDIGLPPVDES LRNEGHGQPVSFEYIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRRQIIIVMPAANYIVAGGSRQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRRQIIIVMPAANYIVAGGSRQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQLKEAFKAE PVAAGKEX					
m750	QAAEQLKAAFKAE PVAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```
1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CGGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTTGGTC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTATTGCA
301 GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTTCCTGAA CTGATGTATG
401 TCGGTTACGA CCAATTAAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTTCAG AAAAACTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
501 GGGTAACGGC TGGTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGCTA TTGCGATAGC AGTTATTTTG
851 CGGAGGTGCC AAAAGCAGGT ACAAAGAAT TTGATGACTA TGTAAAAATA
901 TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAAACTTAA
951 ACCCATACTG GTAGAACCAA ACAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCTTT CTA
```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

```
1  MAWSMFATTQ ADRAVRSATA PKEMWFHKKI IDEKTGKVSF DTRQIWSLND
51  LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAKQNR NSTNGSGVIA
101 VMNPPTGKYK SDSNNKIKDF LWLGSSLVSE LMYVGYDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVQKMNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFGVGNKWIPF LLGTNDTTQG TCKGLCYSHS SYFAEVPKAG TKEFDDYVKI
301 WGEVEYDAQG KPINKSKPIL VEPNKTCDNE KYEKEAF*
```

a751.seq not found yet

a751.pep not found yet

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g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

```

m752.seq..
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAATGATT TTGGATTGCG ACCGCATTGC
651 TACCACTAAG GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTGCAATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCCTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGCTCT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTG GAGCACTACA TTTCCGACAA ACAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```

m752.pep
1  MKISRPEFT LLQOYMOHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAIIILHE LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFYIYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

```

m752-1.seq
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAATGATT TTGGATTGCG ACCGCATTGC

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```

651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGTTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTG GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRELLKSLIM
151 EEAITSQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRODDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFIYYQC DIIKRAVDL EHYISDKQKH QOEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDL SKL GEYRFLVPPF
451 SGNALFYVAP QDLLEKLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTTAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTCG GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTTCTTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGG AGCGATAAGG GTTTGAGAA TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAI WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLED RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

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g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```

m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTTG GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCCACAG
451 GTTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCTG CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAAATG ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```

m754.pep
1  MMKSILTVSG NMRKPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRCND PLENEWIDGL EMKNPRILTE RDLIGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDT SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKPTY PSKNTLLDFA EKYCDLGRED ASEMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*

```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```

m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTAACACCA
101 TCTTGGCTAG ACATGGATT TTTGAAATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTTACC
251 GCCTTGAAAG TGATTTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAACACAG CTTTCCTTCA ACGTGTGTA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTTGAATT GGAAAGTCTT AACCTGAAAT TAAATTAA

```

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This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

```
m755.pep..
  1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSSVYLQ
  51 REGISEAHGT IAIQELTARF DWFYSCISNI KEYRLESDLN AQFIADGVYQ
 101 AKQAFQORVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

```
m756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

```
m756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

```
a756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

```
a756.pep
  1 MTANFAQTLV EIQDSLXRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

```

          10      20      30      40      50      60
m756.pep MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE
          |||
a756      MTANFAQTLVEIQDSLXRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE
          10      20      30      40      50      60
```

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	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

```

m757.seq
1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAATAAAC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAAACTG TCCTAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGGCG ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

```

m757.pep (lipoprotein)
1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPQKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPVS VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

```

m758.seq
1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGTGGAAATT CCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCCGGTC GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGAGAAA GGATTGAGCC
501 ATGA

```

1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVPFFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAAC TGTGGAATTT CCCGCTGCTG ACGGCGGCGA ATACGGCCCG
151  GATTTGGCGG AAGTCGCTGC TTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCCGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVPFFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

	10	20	30	40	50	60
m758.pep	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ					
a758	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ					
	10	20	30	40	50	60
m758.pep	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
	70	80	90	100	110	120
m758.pep	130	140	150	160		
	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTCCCTG CTTACTCATC CATTGTCCGC AACGATGTCG
101  ATTACCAATA TTTTCGCGAC TTGCGCGAAA ATAAAGGCGC GTTACCCGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201  GGTTCCTAAC GGCATCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAAGC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401  ACGACTACCA CCTTCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGA AACGGCCAGC CAAAGGCCAA
501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTGTACGA CTCGGCTCAG
551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG
601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA
651 AAACCACGGC TTA CTCTGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTTTCGACAAG
751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGGCTT
801 CGATAATTTT TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCTGGCT GACCACCAAC
901 GAACTCATAT GGCGCGACAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
951 CAACGAACGC ATCACCTGTC CCATTGCAAA CCCTTCGCTT GCCCCACAAA
1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
1101 AGGCGCAGGC GCATTGCAGT TCGACAGCAA CTTACCGTTC GTCCGTAATA
1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC
1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGGCG
1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA
1301 TCGGGGAAGG CACTGTCTGA CTCGCCCAA AAGCTGCTTC AGACGGCAGC
1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
1401 CCTCGCGAC AGCCAGCAA TCAAACCGA AAACCTCTAT TTCGGCTTCA
1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC
1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC
1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCTG
1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTTACGAA
1651 TACATCAACC CGCACCGCAA CCGTCGGACC GACTACTTCA TACTCAAACC
1701 CGGCGGCAAC CCGCGCGAAT TTTTCCCGTT AAATATGAAA AACTCAACAA
1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC
1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAG AAAACCAATG
1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC
1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
2001 ACGCACCGAC AGCACGCTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG
2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC
2101 CATGCTTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC
2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCCG
2351 TTTTAAAAGC CGAAAACATAT CGTGCACTAC CTGCAACGCA AGTACGCGGC
2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
2551 GACGCGCAC AAATTACCCT GAACCCGAT TTCGCCAATA ATACACAA
2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTTCGCA
2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
2701 AAAGTGAAG GGGACAGCCG CGGCGCATTC CAAATCCAG TCAAAAACAC
2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCACTGTG AGCCTCAATC
2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT
2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAA AACAAACAG GATACAGCCT
2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCGTGCGG
2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
3151 CGTGCCCAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
3201 TCAGGTTGCC AAAGCCGCGC ACACGAACGA CCTGACACTC TTCGAAACCG
3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC
3301 AAAGCACGGC AAGGCGCGA TCGGCAAGCC GTCGAAACAG CCCGGCACGC
3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAATCCAC AGTTTGAAAA
3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAAT GATCAGCCGG
3451 TCGGCCAACA CCGCCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA
3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
3551 ACATCTGGCT GGAAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
3601 CACCGTCCCT ACCAACAAAC TACCAACTAT GCACATATCG GCATCCAAAC
3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA
3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

1234

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCC GCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCGCCAC AAACAGGCAG GAATCAAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
1 MRFTHTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
51 GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQE YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTDREFFYFVR LSGGTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIROYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNSDRHP SEDAGKTLLI
351 SSRFDNKTLM LADNINQGAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAGTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGRLDL NGNNLAFTHI
501 RHADGGAQIV NHNPDAQATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAYVG
651 RPEYRYNGAL NLHYRKPRTD STLLNNGGMN LNGEVLIEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQGKTECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNRSEL RLGKAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALTL
851 DGAQITLNPD FANNTNHNRF NTLTVNGTLD GFGTFRFLTG IVRKQNPAPL
901 KLEGDSRGAF QIHVKNTGQE PQTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQQ AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEISR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQQNIWLETG TQQTDYHSGT
1201 HRPYQQTNY AHIGIQTGIT DRLSVGTILT DERTNNRFE GVSARNRSG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTHW AGIRLDKIVE
1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQAAGT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
1 AACAAACGCA ACACCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTACAG CTATCTGCAC AGCCAAATCA AAACGCGCGC CAATCCACGC
151 GACGACGGCA TCTTCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
1 NNRNTRYAAL GKRVMEGVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
51 DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

1235

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1   ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAAAGCGG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCAGC CTGCCCAACC TGTTCCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGTCTCT CCGTCCCCTC CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGCT ATCTTTACCA GCAACGCGCG CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTTAAATGC ACAGCCACGA CGTGTTCGCG
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGC CTTTGCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAGGTTT GTCGTTGATT
1351 GCAGCGGAC GTGTAGGACA TCACAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCTC CCAACTCTAC
1501 ACACCGCAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCTG TACGCCGAT TGGGCAAACG
1701 CGTGATGGAA GGTGTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTCCTG CTGATGCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC
1951 GGTATGCGCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAC
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCCC
2051 GCGTCGGCAG CGAGAGCACC TTAAACATT CCGGTTGCGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1   MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPKA FQGHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDIVL
251 GAGYLYQORR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSHDVFA
301 DLKHYFGNGG YGKVMGRYSR RKADSNYTFA GSKLNNTGQA DVAGLGTDIK
351 QKAFVADASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSKVALD
401 GFRALPYNGI LQNRARAGNK FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSEERSL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSFYRMKDKNAAAPLDSNNKTRYAALGKRVMEGVETEISGAMTPKW					
				10	20	30
g760	NNRNTRYAALGKRVMEGVETEISGAITPKW					
	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
	40	50	60	70	80	90
g760	QIHAGYSYLHSQIKTAAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYYARVGSESTFNIPGSERSLTANL					
	100	110	120	130	140	150
g760	AGMHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYYARVGNTNIPGSERSLTANL					
	709					
m760.pep	RYSFX					
g760	RYSFX					

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq

1	ATGAAAATAT	CATTTTCATTT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTITTC	TGCGCGGTTT
351	TCAAGCGCAG	GCATCCGATA	TTTACCGCGA	CGGCGTGCGC	GAAAGCGGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAAACG	TCGCCATCCG	TCTCACCGGC	GAAAGTCGGC	GCGCCAATTC
651	GTTCCGCAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATTAA
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCGA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACCGCA	TGGGGTTTCG	CCACCGGAAC	GATTTTGTCA
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTTGAA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTTC	AGCAGCGCCT
1151	TTTCCGCTTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCGATTTC	AAATTCTGTC
1301	TCGGCGGCGG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACCTACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTCAGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTTGAGCAT	CGATACGTTG
1501	TCTTCGCGCC	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGGCGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA

1237

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACCTAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGTAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

m761.pep

```

1 MKISFHLALL PTLIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQOTD NKTLSNLTLL
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPAPYG RGGYLSIDTL
501 SSAFVNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

a761.seq

```

1 ATGAAAATAT CATTTCATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCTGTT GCTGCCGCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCGC CCTACGATAT GCGCGCGGAA AGCATTTTCC TCGCGGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACCG GAAACGCGGC
401 AGGTGCGCGC TAGCACC GCC ATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCTCCG TGCTTTATGG GCGTACCAAC GGGCGCGGTG TCATCAACAT
501 GGTCAAGCAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTTCGTG GGCAAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTCACC GGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT
701 CCGTCAAAT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCCGACTG CCTTACCGCA TGGGGTTCCG CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCGGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCAGCGCGG CGCAGGATTT
951 TGATCATTTC TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAT
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTAA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCGCTCT CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTGCTCC
1301 TCGCGGCGG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGCGGGCT ATTGAGCAT CGATACGTTG
1501 TCTTCGCGCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGGA TCCAAAAAAC
1651 AACCCTTATA TTTATGCGGT TAGCGGCAAA ACCCGTTCG CCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1  MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51  KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVS K YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFHRND FVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTND NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQIPILQNR HKADSYGIFV QNIFSATPDL KEVLGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMQA KVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

m761.pep	10	20	30	40	50	60
a761	10	20	30	40	50	60
m761.pep	70	80	90	100	110	120
a761	70	80	90	100	110	120
m761.pep	130	140	150	160	170	180
a761	130	140	150	160	170	180
m761.pep	190	200	210	220	230	240
a761	190	200	210	220	230	240
m761.pep	250	260	270	280	290	300
a761	250	260	270	280	290	300
m761.pep	310	320	330	340	350	360
a761	310	320	330	340	350	360
	370	380	390	400	410	420

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```

m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
a761      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
           370      380      390      400      410      420

           430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
a761      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
           430      440      450      460      470      480

           490      500      510      520      530      540
m761.pep  YNKGFAFYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
a761      YNKGFAFYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
           490      500      510      520      530      540

           550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761      NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
           550      560      570      580      590      600

           610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYSNRNKEVTTLPGFARVDAM
a761      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
           610      620      630      640      650      660

           670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761      LGWNHKNVNVTFAAANLFNQKYWRSDSMPGNPRGYTARVNYRFX
           670      680      690      700

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g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTC GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGCG
201 AATTATTTAT CCTATTTTAT ATTTTITTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTATGAG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1   MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LFLLEIFNEV TKSIIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTC GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGCG
201 AATTATTTAT CCTATTTTAT ATTTTITTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAACCGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTCCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSEF DLLVQLCTIL FHSQKIYFIT
51 LFLLFIFNFV TKSIIYMAIIY PIIYFFTIKK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIINFFSLLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GCGCGAGCAA CATTTCGGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG
251 CAGTGC CGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT CTTCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTGACCGTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CCGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACCGG TATTTGCGGA
1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGSTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTGCGCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GCGCGAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTGTC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGGCG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACAGTGT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTGCG CGCTTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAGACA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACC GGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACGCG TATTTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

m763.pep      10      20      30      40      50      60
               MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a763          10      20      30      40      50      60
               MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT

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	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSAD	FQASHYQRDAV	RRARQQQAKA	AFPHV	SANASYQRQPP	SISSTRETQ
a763	LPEAWRAAQHSAD	FQASHYQRDAV	RRARQQQAKA	AFPHV	SANASYQRQPP	SISSTRETQ
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLF	DAAKFAQYRQSR	FDTQAAEQRF	DAAREELLK	VAESYFNVLL	SRDVTAA
a763	GWSVQVGQTLF	DAAKFAQYRQSR	FDTQAAEQRF	DAAREELLK	VAESYFNVLL	SRDVTAA
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQ	VRQAQALFNK	GAATALDI	HEAKAGYD	NALAQEI	AVLAEKQTYENQLNDY
a763	HAAEKEAYAQQ	VRQAQALFNK	GAATALDI	HEAKAGYD	NALAQEI	AVLAEKQTYENQLNDY
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TDLD	SKQIEAIDTAN	LLARYLPK	LERYSL	DEWQRI	ALSNNHEYRMQQLALQSSGQALRAA
a763	TGLD	SKQIEAIDTAN	LLARYLPK	LERYSL	DEWQRI	ALSNNHEYRMQQLALQSSGQALRAA
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSA	HVGYQNNLYT	SSAQNN	DYHYRGK	GMSVGVQ	LNPLTYTG
a763	QNSRYPTVSA	HVGYQNNLYT	SSAQNN	DYHYRGK	GMSVGVQ	LNPLTYTG
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQ	LATERHIK	LAVRQAY	TESGAARY	QIMAQ	ERVLESSRLKLKSTETGQQYGIR
a763	QYGAAEAQ	LATERHIK	LAVRQAY	TESGAARY	QIMAQ	ERVLESSRLKLKSTETGQQYGIR
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQ	EVAQAEQK	LAQARYK	FMLAYL	RLVKES	GLGLETVFAEX
a763	NRLEVIRARQ	EVAQAEQK	LAQARYK	FMLAYL	RLVKES	GLGLETVFAEX
	430	440	450	460		

1243

g764.seq not found yet

g764.pap not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```

m764.seq
1   ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAAGT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GGCCTTTTTG CCCGCGCATT TGGAACGTAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGGCAA AACGGTGTCT GCGGCGCGCA GCAAACCATC CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CCGACGCGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GCGCATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CCGGCCGACA ATTTTATTTC GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGT GCTGAATACG CAGAACTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CCGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGTG GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG CCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GGCGGTGCTG GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```

m764.pap
1   MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAFLE PAHLELTDTF
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDQHVHQGE TLAELEAVGT DSDVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE OKLVSVGAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRQQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGLTGT
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```

a764.seq (partial)
1   ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAAGT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GGCCTTTTTG CCCGCGCATT TGGAACGTAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGGCAA AACGGTGTCT GCGGCGCGCA GCAAACCATC CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CCGACGCGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GCGCATCGAG CAGCAGAAAA

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701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAAT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
  1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAFLE PAHLELTDTP
 51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQALRGHQ AELQSAKAE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
a764	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
a764	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
m764.pep	130	140	150	160	170	180
	TLAELEAVGTDSDVVQSEQALQAAQLSKLRYEAVLALESRTVPHIDMAQARSLGLSDAD					
a764	130	140	150	160	170	180
	TLAELEAVGTDSDVVQSEQALQAAQLSKLRYEAVLALESRTVPHIDMAQARSLGLSDAD					
m764.pep	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQALRGHQAEQKLVSVAIEQQKTADYRRL					
a764	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQALRGHQAEQKLVSVAIEQQKTADYRRL					
m764.pep	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
a764	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
m764.pep	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
a764	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
m764.pep	370	380	390	400	410	420
	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVDHAVSHEQLGLVYT					

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```

a764      |||||
          DKMDVEVLVLNKGDFVEQGDVAVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
          370      380      390      400      410      420

          430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
          |||||
a764      AVVSLDKHTLNIDGK
          430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT GCGGTCCGAA ATCCGTTTGG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTCACGGT CATGATCCG CCACAATGAA
201 CGCTGCGGCT GCCAAGATT ATATGAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACCGGTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTGG GGACGTACGG
651 TCTTACCTTG CTTATAGCC GCAGCTTGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAAACGGCT TTATTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```

m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVVG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEIAAI MGHEMTHALH EHGKKNVGGQ ILTNTAAQIG TQILDKKPD
201 TNPELVGLGM DILGTYGLTL PYSRSEEEA DEGGMLMAQ AGYHPAAVR
251 VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLLEPTVM PVYEQSVRNK
301 GRVNNKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT GCGGTCCGAA ATCCGTTTGG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTCACGGT CAGGATCCG CCACAATGAA
201 TGCTGCGGCT GCCAAGATT ATATGAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACCGGTGGG
401 CAATGCCCGG CGGAAAAATG GCGTTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTGG GGATGTACGG
651 CATTACCTTG CTTATAGCC GCAGCTTGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAAACGGCT TTATTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```

a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG

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51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEGIAAI MGHEMTHALH EHGKKNVGQK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSL EEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITs THPTNNARIE NLKRLLPTVM PVYEHsVRNK
301 GRVKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

```

              10      20      30      40      50      60
m765.pep      MLRCRPKSVLSDGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACAVVADVYG
              |||||
a765           MLRCRPKSVLSDGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACTVVADVYG
              10      20      30      40      50      60

              70      80      90     100     110     120
m765.pep      HDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTSHKFDW
              :|||
a765           QDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTGHKFDW
              70      80      90     100     110     120

              130     140     150     160     170     180
m765.pep      KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHEMTHALHEHGKKNVGQK
              |||||
a765           KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKKNVGQK
              130     140     150     160     170     180

              190     200     210     220     230     240
m765.pep      ILTNAAQIGTQIILDKKPDNTPELVGLGMDILGTYGLTLPYSRSL EEEA DEGGMMLMAQ
              |||
a765           ILTNAAQIGTQIILDKKPDNTPELVGLGMDILGMYGITL PYSRSL EEEA DEGGMMLMAQ
              190     200     210     220     230     240

              250     260     270     280     290     300
m765.pep      AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPTVMPVYEQSVRNK
              |||||
a765           AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPTVMPVYEHsVRNK
              250     260     270     280     290     300

              310
m765.pep      GRVKNRRRX
              |||||
a765           GRVKNRRRX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTT GTGGATAAAC
101 CCATTCTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTCGGC
151 TATTTTTCGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGT TTGGAACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAAGTTT TGACGGCAAA AAACGTATGC GCGCCTATGA TTCCCCCGAA
451 GCTGCCGCCG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAGAATT GGTTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
51  YFCVCHHFFD PLLKLKGLAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANSV FKAUYEQKIR LENRAVAGKW ALSQKGFDDK KLMRAYDSPE
 151 AAAVALKMQK LTEQYGDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AGAACAGTCG GGTAATAATTG AGGTTTGTGA ATTTTTCGGC
 151 TATTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAACTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CCGCTGCCGT CAATTTGTCTG
 301 GGTTTGAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAACA GGTCTGTTGC CGGAAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AAATGATGC GCGCTATGA TTCCCCCGAA
 451 GCTGCCCGC CCGCATTAAT AATGCAGAAA CTGACGGAAC AATACCGCAT
 501 CGACAGCAG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
 551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGATT GGTGCCAAA
 601 GTCAGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
 51 YFCVHCHHFD PLLKLKGLAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
 101 GLKYQANPAV FKAUYEQKIR LENRSVAGKW ALSQKGFDDK KLMRAYDSPE
 151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPQEQS	GKIEVLEFFG	YFCVHCHHFD
m767						
	10	20	30	40	50	60
g767.pep	PLLLKLGKAL	PSDYLRT	EHVVWRPE	MLGLARMA	AAVNL	SGLKYQANS
m767	PLLLKLGKAL	PSDYLRT	EHVVWRPE	MLGLARMA	AAVNL	SGLKYQANS
	70	80	90	100	110	120
g767.pep	FAVFKAVYEQKIR					
m767	FAVFKAVYEQKIR					
	70	80	90	100	110	120
g767.pep	LENRAVAGKW	ALSQKGFDDK	KLMRAYDSPE	AAAVALKMQK	LTEQYGDST	PTVIVGGKYR
m767	LENRSVAGKW	ALSQKGFDDK	KLMRAYDSPE	AAAVALKMQK	LTEQYRIDST	PTVIVGGKYR
	130	140	150	160	170	180
g767.pep	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
m767	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
	190	200	210			
g767.pep	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
m767	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AAAACAGTCG GGCATAATTG AGGTTTGTGA ATTTTTCGGC
 151 TATTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAATGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCAAGAATGG CTGCTGCCGT CAAGCTGTCA
 301 GGTTTGAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAACA GGTCTGTTGC CGAATAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AAATGATGC GCGCTACGA CTCTCCTGCG

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451 GCAGCGGCTG CTGCATCAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCGCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
  1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPKQOS GKIEVLEFFG
 51 YFCVHCHHFD PLLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAVYEQKIR LENRSVAEKW ALSQKGFDDG KLMRAYDSPA
151 AAAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

	10	20	30	40	50	60
a767.pep	MKLKHLLPLL LSAVLSAQAYALTEGEDYLV LDKPIPKQOSGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLLPLL LSAVLSAQAYALTEGEDYLV LDKPIPKQOSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
a767.pep	PLLLKLKALP SDAYLRTEHVVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEQKIR					
m767	PLLLKLKALP SDAYLRTEHVVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEQKIR					
	70	80	90	100	110	120
a767.pep	LENRSVAEKWALSQKGFDDGKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKYYR					
m767	LENRSVAGKWALSQKGFDDGKLMRAYDSPEAAAAALKMQQLTEQYRIDSTPTVIVVGKYYR					
	130	140	150	160	170	180
a767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
  1 ATGAATATCA AACAAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCACGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGCGGTTAT GAAGACCTGC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
  1 MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQHSAVVI DVRSEQEFSE
 51 GHLHNAVNIPTVDQIVRRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
  1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

```

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHNLHNAVNI VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSAVWI	DVRSEQEFSE	GHNLHNAVNI
m768	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSAVWI	DVRSEQEFSE	GHNLHNAVNI
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VDQIVRRIHE	AAPDKDTPVN	LYCRSGRRAE	AALQELKKAG	YTNVANHGGY	EDLLKKGMMK
m768	VDQIVRRIHE	AAPDKDTPVN	LYCRSGRRAE	AALQELKKAG	YTNVANHGGY	EDLLKKGMMK
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCGC AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATTACAG CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCGC
 201 CATACACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
 51 GHNLHNAVNI VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSVWI	DVRSEQEFSE	GHNLHNAVNI
m768	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSVWI	DVRSEQEFSE	GHNLHNAVNI
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRRIHE	AAPDKDTPVN	LYCRSGRRAE	AALQELKKAG	YTNVANHGGY	EDLLKKGMMK
m768	VDQIVRRIHE	AAPDKDTPVN	LYCRSGRRAE	AALQELKKAG	YTNVANHGGY	EDLLKKGMMK
	70	80	90	100	110	120

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1  TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAagaAAC ACCgtgCGAA CCGGATTGA GAAGCCGTCC CGAGTTCAGG
151 CTTTCATGAAG CCGAGGTCAA ACCGATCGAC AGGAGAGAAG TACCGGGGCA
201 GGTGCGGGAA AAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCTG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGCGAGGGT GAAGGAGGCG GTTTCCTTAT ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATGTGTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTA AAC GCGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAAAT GGTGCTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
801 CGTGTCGGCG AGGGTTTATC CGGGGAATAA GAAATTCACG GATATGACGG
851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCACGGCG GCACGCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGCGGTT TGAAGAATAC CGCGCGGGCG
1051 CGTTCGACGA ATACCCATTT GCAAATTTCC AATTGCTGGT TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CCGGCGGTTT GGATTTTAC CGCGAGCGCA
1151 ACCCCGCCGA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCAGG AATGGGGCGG CAGCGGCTGT TCTTCGCTGT TCCGCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAGC AGTTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCCG CGCCTGACGC GTGCGCACCG
1401 CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1  LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRO NEAAADQFDR LKTEDLPQOL MEQVELYRKA
201 LRERDAWKVN GGFSVTREHN INQAPKQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNRWQT PRWQTLSSAE WGRKKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRVGLRFA
401 WQGEWGGSL SSLFRLGVAK RHYEKPFFS SFRGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNOVFNEYEK NRAFEVFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

n769.seq

```

1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCTGCACG
51  AAACAGATGG ATGCTGTGTC TGCTTTTATT GGCAGGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACC GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGCAGGT
201 GCGGGAAAAA GGAAGAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCTCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGCGC CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTTACC GGAATTGAT TGCGGCCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCAGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACAGTT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG
601 CGCGAAGCGG ATGCGTGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG CGGCGCAGCT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTTGCCGACC GCGCGAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTCCAAT TCCTGCTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCAG GAGCGCAACC
1151 CCGCCGACCG GGGCGACAA TTAACCGTT ACAGGCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCG CCGCCTGTCT TCCTGTTGCG GCCTCGGCGC

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1251

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1251 GGC GAAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCAGCA
1401 AACCGCGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

```

m769.pep
  1 LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
 51 HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKQQYQ KWTFFPKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFWA
401 GQEWGGGSL SLLRLGAAKR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

```

m769/g769 95.1% identity in 492 aa overlap

      10      20      30      40      50      59
g769.pep LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAETPCEPDLRSRPEFRLHEAEVKPI
      |||
m769      LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPI
      |||
      10      20      30      40      50

      60      70      80      90     100     110     119
g769.pep DREKVPQVREKKGKVLQVDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD
      |||
m769      DREKVPQVREKKGKVLQIDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD
      |||
      60      70      80      90     100     110

      120     130     140     150     160     170     179
g769.pep KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAADQFD
      |||
m769      KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAADQFD
      |||
      120     130     140     150     160     170

      180     190     200     210     220     230     239
g769.pep RLKTEDLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNIINQAPKQQYGNWTFPKQV
      |||
m769      RLKAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNIINQAPKQQYKWTFFPKQV
      |||
      180     190     200     210     220     230

      240     250     260     270     280     290     299
g769.pep DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
      |||
m769      DGTAVNYRLGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
      |||
      240     250     260     270     280     290

      300     310     320     330     340     350     359
g769.pep GLAVFHERRTYGNDAYSANGARLYFNWQTPRWQTLSSAEWGRLKNTRRARSNDNTHLQI
      |||
m769      GLAVFHERRTYGNDAYSYTNGARLYFNWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQI
      |||
      300     310     320     330     340     350

      360     370     380     390     400     410     419
g769.pep SNSLVFYRNARQYWTGGGLDFYRERNPADRGDNFNRYGLRFAWQGEWGGGSLSLFLGVA
      |||
m769      SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWQGEWGGGSLSLRLGAA
      |||
      360     370     380     390     400     410

      420     430     440     450     460     470     479
g769.pep KRHYEKPGFSSFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
      |||

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```

m769      KRHYEKPFFSGFKGERRRDKELNLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
           420      430      440      450      460      470

           480      490
g769.pep   KNRAFVEFNKTFX
           |||||
m769      KNRAFVEFNKTFX
           490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTT TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCATTACC GGAATTGAT TGTCGCCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCGGCAT TGTTTAAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGGG ATGCGTGGAA GGTAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCGTTCG CTTTGCTTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 GCGCAACCGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTTAAAGGGG
1301 AAAGCGCGAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCCA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGCTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLLPLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GVLQIDGET LLKNPELLSR AMYSVVNSN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVMRML AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKROQYG KWTFFKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 QQEWGGSGLS SLLRLGAAGR HYKPGFFSG FRGERRRDKL LNTSLSLWHR
451 ALHFRGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

           10      20      30      40      50      60
a769.pep   LIMVIFYFCGKTTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
           |||||
m769      LIMVIFYFCGKTTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
           10      20      30      40      50      60

           70      80      90      100     110     120
a769.pep   ERVPQVREKGVKVLQIDGETLLKNPELLSRAMYSVVNSNIAGIRVILPIYLQQAQQDKM

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|||||
m769      EKVPGQVREKGVQLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
          70      80      90      100     110     120

          130     140     150     160     170     180
a769.pep  LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
          |||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDAFAVRMRLAAALFENRQNEAAADQFDRL
          130     140     150     160     170     180

          190     200     210     220     230     240
a769.pep  KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNNINQAPKROQYGKWTFFPKQVDG
          |||||
m769      KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNNINQAPKROQYGKWTFFPKQVDG
          190     200     210     220     230     240

          250     260     270     280     290     300
a769.pep  TAVNYRLGAEEKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
          |||||
m769      TAVNYRLGAEEKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
          250     260     270     280     290     300

          310     320     330     340     350     360
a769.pep  AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRCLKNTRRARSNDNTHLQISN
          |||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRCLKNTRRARSNDNTHLQISN
          310     320     330     340     350     360

          370     380     390     400     410     420
a769.pep  SLVFYRNARQYWMGGLDFYREERNPADRGDNFNRYGLRFAWGQEWGGGSLSLRLGAAKR
          |||||
m769      SLVFYRNARQYWMGGLDFYREERNPADRGDNFNRYGLRFAWGQEWGGGSLSLRLGAAKR
          370     380     390     400     410     420

          430     440     450     460     470     480
a769.pep  HYEKPGFFSGFKGERRRDKEKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
          |||||
m769      HYEKPGFFSGFKGERRRDKEKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
          430     440     450     460     470     480

          490
a769.pep  RAFVEFNKTFX
          |||||
m769      RAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGCGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCG CTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGT TCGTGC GTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AGCGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTTCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCGATA AAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACSGSE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KGGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKRGTFEA FKSRIQVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FSGIPQTDG VQADTSGKLL AGACIIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGCGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

m770.pep

```

1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKS RQIVRY DPKRKTFAYL VYSDKIIQS PKNLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

	10	20	30	40	50	60
g770.pep	MNRLLLLSAAVLPTACGSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
g770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKKEVFKRGTFGFAFKSRQIVRY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKKEVFKHGASFAFKSRQIVRY					
	70	80	90	100	110	120
	130	140	150	160	170	180
g770.pep	DPKRKAFAYLVYSDKIVQSGPKNLSAVSCFGSGIPQTDGVQADTSGKLLAGACIISNPI					
m770	DPKRKTFAYLVYSDKIIQSGPKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
g770.pep	KNPDKRX					
m770	ENLDRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

a770.seq

```

1 ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51 CAGCGGGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCTCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

a770.pep

```

1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKS RQIVRY DPKRKTFAYL VYSDKIIQS PKNLSAVSC

```

1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap.

	10	20	30	40	50	60
a770.pep	MNRLLLLSAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDPPDVQGVACYISYA					
m770	MNRLLLLSAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDPPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKEVFKHGASFAFKSRQIVRY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKEVFKHGASFAFKSRQIVRY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRRTFAYLVYSDKIIQGSFPKNSLSAVSCFGGGIPQTDG VQADTSGNLLAGACMISNPI					
m770	DPKRRTFAYLVYSDKIIQGSFPKNSLSAVSCFGGGIPQTDG VQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPKRXX					
m770	ENLDRXX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGCTGACG	ATGCTGCTTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCTT	CACGCCCGAA	AACATCCGCA	GCCGCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAT	CTCGTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCGC	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGGCG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCGGAT	CTTGCCCTGA	CGCGCGACAG	AAACGCGGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTC	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTCTGTC	GGGCAGCAGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGAGAA	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCAGCGCCG	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	CCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCGCAAAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCTT	CAAACCAATT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGGAGTC	GGGACAACGG	GCTGGACGCC
1051	CCGCGCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCCGTGGCC
1201	GCAAAATTCA	AATATACGCG	GGAAGGCGCA	CCGCACCTGG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAAACC	TCGCCCCCTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCCC	GACATCTTCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	GGGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCTTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTCAATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGCTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CGCGTGGCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCCG

1256

```

1751 GGAAATCTC GGGCAGCACA CCCTTCTACC GATTACGCT CAACAGCGAA
1801 ATTTAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

g771.pep

```

1 MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQOSI
51 ANTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRII
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQOFESSGIL VWRKLSVPWK
201 SRGLFSLDGI GTPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNIS KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGLSI PNLQWNNAEL NGTFDRQPVA
401 AKFKYTRREGA PHLEAAAALO KLNLPYLDE FRQNGKIFP DILGRLSGNV
451 EHLKIGSIQ LPGLQLDDME TYLHADKDH ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTASGENRK
551 QLIRSLQSSL SLNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHID TELFSDSLYV TSNGYTNLDT QELSEDVLR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKPE
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

m771.seq

```

1 ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGCTGACG ATACTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCCTGA AACATCCGCA GCCGCCTACA ACAAGCATT
151 GCACACACAC ACCGAAAAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
201 CCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGAAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGCCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTGTC GGGCAGCCGT
551 TTGAAAGTTC GGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCTTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTC GAAGCTTCCA CTTGCTGGA CCGACACGGC ATTACCATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 CGCGGCCCTG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAATC CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTATCC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCCTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAC ACCCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGGC
1051 CCGCGCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCTCG CCAAGCTGTC CGCGGACATC
1351 GAGCGCACC TGAAAATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC CGCTCAGCC
1451 GTTTCAGTTC AGGGCTTTAC GGCGGCCATA CCGAAGCGCG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCTG CAACAGAATG CAAGCAACAT
1551 CCAAAATCCA CGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1701 TGATATGGAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAACTGCG CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACG
1801 CTCAACAGCG AAATTTTCTA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTCTCTCGAC AGCCTCTATG TTACAGCAAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCC CGCAAAGAGA
2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAAATGGA GTGGCTCAAA
2101 CCTAAAGAAC CGTA

```

1257

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

```
m771.pep
1 MDLLSVFHKY RLKYAVAVLT ILLAAVGLH ASVYRTFTPE NIRSRLQOSI
51 ANTHRRKISFD ADIQRRLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHEAAVALQ KNLTPYLDD VRQONGKIFP DTLAKLSGDI
451 EAHKIGKVQ LPLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS LSNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDQTQELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGIN S RKEKQKILED TLEQWQWLK
701 PKEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

```
m771/g771 90.3% identity in 704 aa overlap
10 20 30 40 50 60
g771.pep MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQOSIAHTRKISFD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQOSIAHTRKISFD
10 20 30 40 50 60

70 80 90 100 110 120
g771.pep ADIRRRLLPRPTVILKNLITITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVSGAD
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 ADIQRRLPRPTVILKNLITITEPGGDQTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE
70 80 90 100 110 120

130 140 150 160 170 180
g771.pep LALTRDRNGAWNIDLFDGAKHSASVNRIIVENSTVRLNLFQQLILKEISNLQSPDSS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNLFQQLILKEINLQSPDSS
130 140 150 160 170 180

190 200 210 220 230 240
g771.pep GQPFESSGILVWRKLSVPWKSRLGLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 GQPFESSGILVWGLSVPWKSRLGLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
190 200 210 220 230 240

250 260 270 280 290 300
g771.pep VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
250 260 270 280 290 300

310 320 330 340 350 360
g771.pep SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSDNGLDAPRLHISTLQD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
310 320 330 340 350 360

370 380 390 400 410 420
g771.pep TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFKYTREGAPHLEAAALQ
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 TVNRLPQPRFISRLDGSLSVPLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
370 380 390 400 410 420

430 440 450 460 470 480
g771.pep KNLNAPYLDEFRRQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDHI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 KNLNTPYLDDVRQNGKIFPDTLAKLSGDIEAHLKIGKVQLPGLQLDDMETYLHADKGHI
```


1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771. pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771. pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG---STPFYRFT					
m771	DLTAGGETRKLIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771. pep	LNSEISDGISRHIDTELFSDSLVYTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLVYTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771. pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

```

a771. seq
1  ATGGATTAT TATCGGTCTT CCACAAATAC CGTCTGAAAT ATGCGGTAGC
51  CGTGCTGACG ATACTGCTTT TGGCGGCAAT CGGGCTGCAC GCTTCCGTAT
101 ATCGCATCTT CACACCTGAA AACATCCGAA GCCGCTCCA ACAAGCATT
151 GCCCATACGC ACCGGAATAA CTCGTTTGAT GCGGATATAC AGCGCAGGCT
201 TCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCG GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGGCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AGACGGCATC GGCACGCCCA AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATTACCATTT
701 CCACCAACCG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAATC CCTACGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCA ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGCG TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACGCCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCC GACCCCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAAAATCGG AAAAGTCCAA CTTCGCCGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTGC AGGGCTTTAC GCGCGCCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTCATC GACCTGACCG CGGGCGGCGA AACC CGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAAACTGC CGAACAATGCC GCACCCAGCA CACCTTCCA CCGATTACAG
1801 CTCACAGCGG AAATTTTACA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTCTCCGAC AGCCTCTATG TTACAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCGGT ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGCG TGACCGGCGG CATCAATTCC CGCAAAGAGA
2051 AACAGAAAAA CCTCGAAGAC ACCCTGCTGG AACATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQQSI
 51 AHTRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKVVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTV
 401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYDD VRQNGKIFP DTLAKLSGDI
 451 EAHKIGKVQ LPGLQLDDME TYLHADKGGHI ALSRFKSGLY GGHTGGISI
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
 551 ELIRSLQGS SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
 601 LNSEISDGIS RHIDTELFSD SLVYTSNGYT NLDTOELSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
 701 PKEP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

	10	20	30	40	50	60
a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPE	NIRSRLQQSI	AHTRKISFD			
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPE	NIRSRLQQSI	AHTRKISFD			
	10	20	30	40	50	60
	70	80	90	100	110	120
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLS	WKNLWSDQIQIEKVVVSSAE				
m771	ADIQRRLPRPTVILKNLTITEPGGDQTA	SVQETKIGLSWKNLWSDQIQIEKVVVSSAE				
	70	80	90	100	110	120
	130	140	150	160	170	180
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQILKEINLNQSPDSS				
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQILKEINLNQSPDSS				
	130	140	150	160	170	180
	190	200	210	220	230	240
a771.pep	GQPFESSGILVWGKLSVPWKS	RGLFLSDGIGTPKISPFHFEASTSLDGHG	ITISTTGSPS			
m771	GQPFESSGILVWGKLSVPWKS	RGLFLSNGIGPPEISPFHFEASTSLDGHG	ITISTTGSPS			
	190	200	210	220	230	240
	250	260	270	280	290	300
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSI	KIETVNGAFTAGGEYAQWDG				
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSI	KIETVNGAFTAGGEYARWDG				
	250	260	270	280	290	300
	310	320	330	340	350	360
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD				
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD				
	310	320	330	340	350	360
	370	380	390	400	410	420
a771.pep	TVNRLPQPRFISRLDGSLSV	PNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ				
m771	TVNRLPQPRFISRLDGSLSV	PNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ				
	370	380	390	400	410	420
	430	440	450	460	470	480
a771.pep	KLNLTPLYDDVRQNGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQLDDMETYLHADKGGHI				
m771	KLNLTPLYDDVRQNGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQLDDMETYLHADKGGHI				
	430	440	450	460	470	480

1260

```

          490      500      510      520      530      540
a771.pep  ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLQDLFGFHSFSGNGDAVI
          |||||
m771      ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLQDLFGFHSFSGNGDAVI
          490      500      510      520      530      540

          550      560      570      580      590      600
a771.pep  DLTAGGETRKEILIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRET
          |||||
m771      DLTAGGETRKEILIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRET
          550      560      570      580      590      600

          610      620      630      640      650      660
a771.pep  LNSEISDGISRHDITELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG
          |||||
m771      LNSEISDGISRHDITELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG
          610      620      630      640      650      660

          670      680      690      700
a771.pep  TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX
          |||||
m771      TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX
          670      680      690      700

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

```

g772.seq
1   GTGTTTCGGCA CGGTCTTGCG GACTGATGCC GACTGCCTGC AAATCATCGT
51  CGTCGGCAAG TTCTTTCAGG TTGTTGCGTA TGGTTTTGCG CGCTTGGCGG
101 AAGGCGAGTT TCACCAAGTTT GCGGAAATGA TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGCAC CACTGCGGAA TCGATTTTCG
201 GCGCGGGATC GAACGATTTCG GCGGCGACGT CAATCAGCAG CTCCATATCG
251 AAAAAATATT GCAGCATCAC ACCCAAGCGA CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATGCGCTCGA CCACTTCTTT TTGCAACATA AAGTGCAAT
351 CGCGGACATC GTCCGCCACC TCCGCCAGTT TGAACAAAAG CGGCGTGAG
401 ATGTTATACG GCAGGTTGCC GACGATTTTC TTTTGCCTG AGATGCCGTT
451 GAAATCAAAC TGCAACACGT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATTG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCC GATAATCCGC GTGTCCTGCA AAAAAATCTG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTCTTCGGT TGAACCCCG
751 CCCTTTAGGG CGGCAGGATC AGACTCTGTT TGGGCGGGGC GTAACCCCTT
801 CCAAAATCAG ACGACACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAACATAAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

```

g772.pep
1   VFGTVLRTDA DCLQIIIVGK FFQVVAYGFA ALAEGEFHQF GEMIEIVRLA
51  DTVFHRNHAH HCGIDFRRGI ERFRHVNQQ LHIEKILQHH TQATVVVAFR
101 RGNHALDHFF LQHKVHIGDI VRHLRQFEQK RRGDVIRQVA DDFLFA*DAV
151 EIKLQHVAHV NHQFIRKRQR FQTAYDVAVD FDNVOAVQLF RQRFGNCRQT
201 RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSSSVETP
251 PFRAAGSDSV WAGRNPFQIR TTHRAVLYVS SCVLEHRCVY SIRLSMSAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

```

m772.seq
1   ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTGCG GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GGCAAAATGC TCGAAATCGT CCGCCTTGCC
151 GATGCGGTGT TTCACCGGAA TCATACGGAC GACGGCGGAA TCCACTTTCG
201 GCGCAGGGTC GAACGATTTCG GCGGTACGT CAATCAGCAT TTCCATATCG
251 AAAAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGCTCGA CCACTTCTTT TTGCAGCATA AAGTGCAAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGTGTGGAA
401 ATGTTGTACG GGAGGTTGCC GACGATTTTC TTTTGCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAAATCTG CCCGAAACGC

```

1261

701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAACT AGACTCTATT TGGGAGGGCG GTAACCTCTT
801 CCAAACTCAG ATGGCACATA GGGCGTGTCG TTATGTGTGC TCTGTGTGT
851 TGAACACATA ATGTGTTTAC AGTATCCGTT TGATGTCCGC ATTGTAA

This corresponds to the amino acid sequence <SEO ID 2660; ORF 772>:

```
m772.pap
1  MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GKMLEIVRLA
51  DAVFHRNHTD DGGIHFRRRV EFRGYVNVQH FHIEKILQHH AQAAVVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 ETKLQYIAFV NHQFIRKQOR FQTAYDVAVD FDNVQAVQVF RQRFGNSRQTP
201 RADFNHDIIR LRAKHVDNIA DNPRLVKQIL PETLAGVFHF HRVSFSRVET
251 PFRAVESDSI WEGRNSFQIR MAHRVLYVS SCVLKHKCVY SIRLSMAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/q772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIIVVGKFFQVVAYGFAALAEGEFHFQFGEMIEIVRLADTVFHRNHAA					
m772	MFAGVLRIDADCLQIIIVACKLFQIVAYGFAALVEGEFHFEGKMLEIVRLADAVFHRNHDT					
	10	20	30	40	50	60
g772.pep	70	80	90	100	110	120
	HCGIDFRRGIERFGRHVNQQHLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	DDGIHFRRRVVERFGRYVNOHFHIEKILQHHAQAADVAFRRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
g772.pep	130	140	150	160	170	180
	VRHLRQFEQKRRGDVIRQVADDFLFXADAVEIKLQHVAFVNHQFIRKRRQFQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLACDAVEIKLQYIAFVNHQFIRKRRQFQTAYDVAVD					
	130	140	150	160	170	180
g772.pep	190	200	210	220	230	240
	FDNVQAVQLFRQRFNGNCRQTRADFNDIIRLRAHGVNDNIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFNGNRRQTRADFNDIIRLRAHGVNDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
g772.pep	250	260	270	280	290	299
	HRVSSSVETPPFRAAGSDSVWAGRNFFQIRTTTHRAVLVYSSCVLEHKCVYSIRLSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVYSSCVLKHKCVYSIRLSALX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2661>:

```
a772.seq
1  ATGTCGCGCG CGGTCTTCGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTCGCAAG CTCCTTTCAGA TTGTTGCGTA TGGTTTTCGG CGGTGGTGTT
101 AAGCGCAGATT TCACGAGATT GGCAGAAATGC TCGAAATCGT CGCCTTCGCC
151 GATACGGTGT TTCACCGGAA TCATCGCGGAC GACGGCCGAA TCCACTTCGT
201 CGCGGGGTCG GAACGATTCC GCGCGCACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CGGTAGTCGT TGCTTTTCGG
301 CGCGGCCAAC ATACGATCGA CCACCTCTTT TTGCAGCATA AAGTCGATAT
351 CGACGACATC GTCGCCCCAC TCCGCCAGCT TGAACAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTTGCC GACGAAATTC TTTTTCGCTG CGATCGCGTT
451 GAATACAAAC TGCATATCAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCGCGCT TTCAGACGG CATACCATGT CGCGGTTCAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTT GCCCAAGGTG TCGGTAAATCG CCGCCAAACG
601 CGGACCGGAT TCAATCAGCA CATATCCGCA CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCTCTGC AAAAATTCGT CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CTTTTCGGT TGAAACCCCG
751 CCTTTTAGGG CGGTAGAAAT AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAATACGAG ACGGCACATA GGGCGTGCTT TATGTGTGTC TCTGTGTGTT
851 TGAACACATA ATGTGTTTAC AGTATCCGTT TGATGTCCGC ATTGTGAA
```

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
  1 MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
 51 DTVFHRNHAD DGRIFHRRGV ERFGRHVNOH FHIEELQHH AQAAVVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGVVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVOLF RQRFGRNRQT
201 RTDFNNDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

m772/a772 95.6% identity in 298 aa overlap

	10	20	30	40	50	60
a772.pep	MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD					
m772	MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a772.pep	DGRIFHRRGVVERFGRHVNOHFHIEELQHHAAQAAVVVAFRRGNHTIDHFFLQHKVHIDDI					
m772	DGGIFHRRRVVERFGRYVNOHFHIEKILQHHAAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a772.pep	VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD					
m772	VRHLRQLEQKRCGNVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a772.pep	FDNVQAVQLFRQRFGRNRQTRTDFNNDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGRNRQTRADFNNDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
	250	260	270	280	290	299
a772.pep	HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
  1 ATGGGATTGG GTGCAACGAC TTTGTGCGGT TCGGGTGCTA TAGGCCGAGG
 51 TCTGTGCAGT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAACTAG
251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATTGGG AAACCTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
451 GCAAGGTTAC CTAAAAATTT TAAAAATTTT GATTATTTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTCTGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAA CAGCGCGAAA TCCATCTGGC CATACCGCA CAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pap
1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TOASEGSRL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101 TGVKTSLTPK TADVQRNLS QSEVGIKWK GIEGQGPWE DYVGKGLSAN
151 ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKEPOL YSTMKGVIDK
201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSO
251 NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAAATGTTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251 CTTCCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA AACTATCAA AACGGCAGGT
401 TTTCTGCCGC AGCCGCCCTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAGCA GGGCGCGTAT
501 GGGGAAGTGT GAATCTGTCA TCGAAATCGG AGGCGGTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TACGCAAAAC ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pap
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTOENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEM NGKVKALEHT KIHPSGRITYV QKLDRLKE
101 HYLNTGEGSA SAHTVETAQN LYNQALKHYQ NGRFSAASAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCGCCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAAACCTTA AACGGCAAG TCAAAGCACT GGAACACGCA AAAACACATT
251 CTTCCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA AACTATAAA AGCGGCAAGT
401 TTTCTGCCGC TGCTCCCTG TTGAAGGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TCGCAAAAC ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pap
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDRLKE
101 HYLNTGEGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCASVLPVPEGSRT	EMPTQENASDGIPYPVPTLQDRLDYLEGKI				
m774	MKIKLPLFIIWLSVSASCASVSPVPAGSQTEM	STRENASDGIPYPVPTLQDRLDYLEGKI				
	10	20	30	40	50	60
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGR	TYVQKLDLDRKLEHYLNTEGGSASAH	TVETAQN			
m774	VRLSNEVETLNGKVKALEHAKTHSSGR	AYVQKLDLDRKLEHYLNTEGGSASAH	TVETAQN			
	70	80	90	100	110	120
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGG	DGGGSIQSRMYLLQSRARMGN	CESVIEIGGRY			
m774	LYNQALKHYKSGKFSAAAALLKGADGG	DGGGSIQSRMYLLQSRARMGN	CESVIEIGGRY			
	130	140	150	160	170	180
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQ	QKDIARATWRS	LIQTYPGSPA	AKRAAAV	RRKRX	
m774	ANRFKDSPTAPEAMFKIGECQYRLQ	QKDIARATWRS	LIQTYPGSPA	AKRAAAV	RRKRX	
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

1	ATGAAGACCA	AATTACCGCT	TTTATCATT	TGGCTGTCCG	TATCCGCCGC
51	CTGTTCTTCC	CCTGTTTCCC	GCAATATTCA	GGATATGCGG	CTCGAACCGC
101	AGGCAGAGGC	AGGTAGTTCG	GACGCTATTC	CCTATCCCGT	TCCCACTCTG
151	CAAGACCGTT	TGGATTATCT	GGAAGGCACA	CTCGTCCGCC	TGTCGAACGA
201	AGTGGAAACC	TTAAACGGCA	AAGTCAAAGC	ACTGGAGCAT	GCGAAAACAC
251	ACCCTTCCAG	CAGGGCATA	GTCCAAAAC	TCGACGACCG	CAAGTTGAAA
301	GAGCATTACC	TCAATACCGA	AGGCGGCAGC	GCATCCGCAC	ATACCGTCGA
351	AACCGCACAA	AACCTCTACA	ATCAGGCACT	CAAACACTAT	AAAAGCGGCA
401	GGTTTCTG	CGCTGCCTCC	CTGTTGAAAG	GCGCGGACGG	AGGCGACGGC
451	GGCAGCATCG	CGCAACGCAG	TATGTACCTG	TTGCTGCAAA	GCAGGGCGCG
501	TATGGGCAAC	TGCGAATCCG	TCATCGAAAT	CGGAGGGCGT	TACGCCAACC
551	GTTTCAAAGA	CAGCCCAACC	GCGCCTGAAG	CCATGTTCAA	AATCGGCGAA
601	TGCCAATACA	GGCTTCAGCA	AAAAGACATT	GCAAGGGCGA	CTTGGCGCAG
651	CCTGATACAG	ACCTATCCCG	GCAGCCCGGC	GGCAAAACGC	GCCGCCGCAG
701	CCGTGCGCAA	ACGATAG			

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

1	MKTKLPLFII	WLSVSACSS	PVSRNIQDMR	LEPQAEAGSS	DAIPYPVPTL
51	QDRLDYLEGT	LVRLSNEVET	LNGKVKALEH	AKTHPSSRAY	VQKLDLDRKLE
101	EHYLNTEGGS	ASAHTVETAQ	NLYNQALKHY	KSGRFSAAA	LLKGADGGDG
151	GSIAQRSMYL	LLQSRARMGN	CESVIEIGGR	YANRFKDSPT	APEAMFKIGE
201	CQYRLQKDI	ARATWRS	LIQTYPGSPA	AKRAAAV	RRKRX*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSACSSPVSRNIQDMR	LEPQAEAGSSDAIPYPVPTLQDRLDYLEGT				
m774	MKIKLPLFIIWLSVSASCAS-VSPVPAGSQTEM	STRENASDGIPYPVPTLQDRLDYLEGK				
	10	20	30	40	50	

1265

```

              70      80      90      100      110      120
a774.pep      LVRLSNEVELNGKVKALEHAKTHPSSRAYVQKLDLDRKLEHYLNTGGSSASHTVETAQ
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774          IVRLSNEVELNGKVKALEHAKTHSSGRAYVQKLDLDRKLEHYLNTGGSSASHTVETAQ
              60      70      80      90      100      110

              130      140      150      160      170      180
a774.pep      NLYNQALKHYKSGRFSAAASLLKGADGGDGGGSIQQRSMYLLQSRARMGNCSVIEIGGR
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774          NLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQQRSMYLLQSRARMGNCSVIEIGGR
              120      130      140      150      160      170

              190      200      210      220      230      239
a774.pep      YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARAAAAVRKRX
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774          YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARAAAAVRKRX
              180      190      200      210      220      230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGGCCCTT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCCG
301 ATCAGCAGCG AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAATC CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACCATC
401 ATACGCATAC GCACAACAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCCG
551 CCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCCG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCCG GTATGCGCCC
651 TCGCGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTCCG
701 TCGCGACCTT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCG GAAGGCAGCA CGATTTTAGG
801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTNH SDADGKALSM
151 RLTPRPLLSR RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMILIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGGCCCTT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCCG
301 ATCAGCAGCG AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAATC CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACCATC
401 ATACGCATAC GCACAACAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCCG
551 CCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCCG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCCG GTATGCGCCC
651 TCGCGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTCCG
701 TCGCGACCTT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

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751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTGAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTCGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
  1 MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
  51 YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
 101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTHNN SDADGKALSM
 151 RLTPRPLLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
 201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
 251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
 301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790 98.2% identity in 342 aa overlap

      10      20      30      40      50      60
a790.pep MARRSKTFEEAAAEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
          |||
m790     MARRSKTFEEAAAEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
          |||

      10      20      30      40      50      60

      70      80      90     100     110     120
a790.pep GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTQAYNEMTKSVAGSNSII
          |||
m790     GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTQAYNEMTKSVAGSNSIV
          |||

      70      80      90     100     110     120

      130     140     150     160     170     180
a790.pep LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSD RQAAAFARTG KLTGSFDLFA
          |||
m790     LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSD RQAAAFARTG KLTGSFDLFA
          |||

      130     140     150     160     170     180

      190     200     210     220     230     240
a790.pep SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID
          |||
m790     SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID
          |||

      190     200     210     220     230     240

      250     260     270     280     290     300
a790.pep IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
          |||
m790     IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
          |||

      250     260     270     280     290     300

      310     320     330     340
a790.pep SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||
m790     SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX
          |||

      310     320     330     340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
  1 ATGTTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTA CTGTTT
  51 TGGTTTGGTT TTTGGTTTGT GTGATTTTGG AGTGGGTCGT GTTGCCATTG
 101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTC TTTGCAGCAT
 151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGCGCGGATG GAGAAGTCAT
 201 CCGTATGTAT GGGGAGCAGC GGCGCGAATT TACAAAAATC GGCGATTTC
 251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
 301 CCGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
 351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCCGCAA ATCTATTCA ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTT GGAATAATCGA
801 TCAGAGTGTG TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCAT ACAGAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCGATC ATCAGAAAGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTGCAT CGCGGCAGCA GCTACCGCGG TCGGAAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCCC GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGACGGCGG GTTGCGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGAG CGGTCGATAA TGAGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAT TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGCG GGCATTATCT AAGGGGATGA
1451 CGCGCTCCAC AGTGGTTAAC GATGCGCGCA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAA ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGGAGGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTCTCGC ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAACG ACAATAAAGA
2001 TCGTGGTTT GTCGGTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 CGGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1 MVNYYSAMIK KILTTCTFLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQFKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLQG RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMPPA VVLDVTKKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPQLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVNV DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQ QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRAGYGGTI
701 AVFVWVDYMR FALKGKQGGK MKMPEGVVSS NGEYYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTGAG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCCGT CTTGGATTTC TTGCGAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCAGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

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451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTGAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC AATAAGATGT CCGAGATTTG
601 ACTTTGCGCG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAGT GCATTACGAG CGGTTTGTTT GGAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TGCGGAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCCCGCC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCAGA GCTGTGCGCG CGCTGGTCGG CGGTATGAT
1351 TTTTACAGCA AAACATTCAA TCGTGCGGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAG GATGCGCCGA TTTCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTCTCGC ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCTGGGCA
1851 AATGACGGCT CAGGCAATCG ATCCGCGCAA TGCCATATAT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACCGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTAA ACCCTGATGT GGTTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTACAGCAG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGCGCGA TGACGAAGTC CGCCAAGATA
2351 TGAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

```

1 MVNYYSAMIK KILTTTCFGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTKRF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKATE ALRKALRNFD RGSSYRGAEN YIDLKSEEDV EETVSQYLSG
351 LYTVDKMPVA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRR AVVQEPLLQG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVNV DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGVAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQ QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVT A YIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVSS NGEYMKERM VTDPLGLDN
751 SGIAPQPSRR AKEDDGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

g791/m791 97.3% identity in 805 aa overlap

```

          10      20      30      40      50      60
g791.pep  MVNYYSAMIKKILTTTCFGLFFGFCVFGVGLVAIAAILVTYPKLPSLDSLQHYQPKMPLTIY
          |||
m791      MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90      100     110     120
g791.pep  SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
          |||
m791      SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
          70      80      90      100     110     120

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	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAGLGPKAPSAYNPIVNPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLGPKAPSAYNPIVNPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKEYGEDAYTQGFKVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKEYGEDAYTQGFKVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDRGSSYRGAENYIDLKSKSEDVEETVSQYLSGLYTVDKMVPA					
m791	RADHOKVATEALRKALRNFDRGSSYRGAENYIDLKSKSEDVEETVSQYLSGLYTVDKMVPA					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDTTKKKNVVIQLPGGRRVALDRLALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
m791	VVLDTTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPQLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPQLQALGSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKINQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKINQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGKQKG					
m791	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGKQKG					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVVSSNGEYYMKERMVTDPLGLDNLNSGIAPQPSRRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYYMKERMVTDPLGLDNLNSGIAPQPSRRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```

1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCGGCGGATG GGGAAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATGGG GGGTGGATGT TTGGGGTGT GCGCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCTTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCCGCGAT
751 CAGGCGTTGA ATGAGGAACG GCATTACGAG CGGTTTGTTC GGAATTCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACCGTGA AGATGCCTAT ACGCAGGTT TTAAGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGAAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CCGCAGCGCG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCGCG CGGTCAATAA TGAATAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTCTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCAAATG CAACCTTGG TGCCCGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGG AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCG TAAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCCC GTATATATCG
2051 GCTTCAGCAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTACGAGC AGTGCGGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC GGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGAGAAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```

1  MVNYYSAMIK KILTTCEGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFFEVLRNA VIAAEDKRFY
101 RHWGVVDVGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTKRF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVROE LYEKYGEDAY TQGFVKYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMPPA VVLDVTKKKK VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVOEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIIT LRQALTASKN MVSIRILMSI GVGYAQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR YSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGQKGG MKMPEGVVSS NGEYMKERM VTDPLGLTLDN
751 SGIAPQPSRR AKEDDGGAEE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVITYPKLPSLDSLQHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVITYPKLPSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAVGNVVS
	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAVGNVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPVNPRAKLROKYILNNMLE
	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPVNPRAKLROKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFVYTTV
	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	RADHQQVATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA
	RADHQQVATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	VVLDTVTKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	VVLDTVTKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	AVVQEPLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	AVVQEPLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLQALTASKNMVSIIRILMSI
	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLQALTASKNMVSIIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	GVGYAQYIIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	GVGYAQYIIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	DRDGRRAQMQLVAGQNAQDAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	DRDGRRAQMQLVAGQNAQDAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	TTNDNKDAWFGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKGK
	TTNDNKDAWFGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKGK
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	MKMPEGVVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV
	MKMPEGVVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX	790	800			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGGAAAGAGC GGCATTACG GCAATGATGG AAGCTGTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AACTCAATC GAATGGCACT ACGGCGtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAACCG GCcgcaGACC
551 TGACcAAACA GCAGgcggcG aaactgacgg tactcgtccc cgccccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggt cgccaaatta ccccaaacgc aaacggactg
701 attgttcag atattgaaat gccgcctgaa ctggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIONAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKPP AADLTQQA KLTVLVPAPF
201 YYSDHPKSKR LRNKTNIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCGCGTTTTCG
251 CCGGGCAGCG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTAC CGACAAAGAC
451 AGGATTTTTC AACTGTATTT AACTCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAATACCC CGCGCCAAGC
551 TGACCAACA GCAGGCGGCA AACTGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1  MFRIIKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIONAIRR
101 NRNSGRVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQA KLTARVPAPL
201 YYADHPKSKR LRNKTNIVLK RMGSAELPES DTD*

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g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASD	VRFAGHGGFD	GDGIONAIRR	NRNSGEVKAG	GSTISQQLAK	

[illegible]

```

a792.seq
1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATTGTT ACGGCAACAT CATTACCTAC GCGCCGTCG
101 CGCCCCATCG GACTGCTTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCATT GGATTACCGT TGGATTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCTTGATTGC TTCGAAGAT GCCCGTTTCG
251 CGGGGACGCG CGGCTTCGAT TTGGGGCGCA TTCAAACGCG CATCATGGCG
301 AACCGBAACA GCGGCAAAAT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAA AACTGTTTTT TAAACGAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC CGCATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTTG AACTGTATTT AAACCTAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA GCGCGTCCCT GGATTTTTTA TCAAATACCC GCCGCCAAGC
551 TGACCAAACA CGAGGCGGCA AACTGACGCG CGCGCGTCCC CGCCCGCTCG
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCGCAACA AAACCAATAT
651 CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC CATACGGACT
701 GA

```

a792.pep

1	MFRIIKWLIA	LPVGIFIFFN	AYVYGNIIY	RAVAPHRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WMPYKRISTN	LKKALIASED	ARFAGHG GFD	WGGIQNAIRR
101	NRNSGKVKAG	GSTISQQLAK	NLFLNESRSY	IRKGEEAAIT	AMMEAVTDKD
151	RFELYLNSI	EWHYGVFGAE	AASRYFQIP	AAKLTKQQA	KLTVRVPAPL
201	YYADHPKSKR	LRKNTINVL	RMGSAAELPES	DTD*	

	10	20	30	40	50	60
a792.pep	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRD	VALDYR			
m792	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRD	VALDYR			
	10	20	30	40	50	60
a792.pep	70	80	90	100	110	120
a792.pep	WMPYKRISTNLKKALIASEDARFAGHGG	FDWGGIQNAIRNRNRNSGKVKAGGST	ISQQLAK			
m792	WMPYKRISTNLKKALIASEDARFAGHGG	FDWGGIQNAIRNRNRNSGKVKAGGST	ISQQLAK			
	70	80	90	100	110	120
a792.pep	130	140	150	160	170	180
a792.pep	NLFLNESRSYIRKGEEAAITAMMEAVTD	KDRIFELYLNSIEWHYGVFGAEAA	SRFYQIP			
m792	NLFLNESRSYIRKGEEAAITAMMEAVTD	KDRIFELYLNSIEWHYGVFGAEAA	SRFYQIP			
	130	140	150	160	170	180
a792.pep	190	200	210	220	230	
a792.pep	AAKLTKQAAAKLTARVPAPLYADHPKSK	RLRNKTNIVLRRMGSAELPESD	TDX			
m792	AAKLTKQAAAKLTARVPAPLYADHPKSK	RLRNKTNIVLRRMGSAELPESD	TDX			
	190	200	210	220	230	

q793.seq

1274

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1  ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTTGTTTGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTGCGATGTG CCGGTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAAGCCT TGGGTTTGGA AAACCTTTGTA TTTGAAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCGTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCGCAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CCGTCAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 CGCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTGCGTAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGGCGGCCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCCGC GCAAGGCAAA CGCATATTCA AAGAATCGAC
1401 CGGCGCGCAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGGC GGTGCGGCTG GACGGTTTCG ATGTCGGCGC TAAAACCGGC
1501 ACGGCGCGCA AGTTCGTCOA CGGGCGTTAT GCCGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCAAAAAA CCCCCTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCCAGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCGGACC AAGCCACTGA CCGCGGCAGC CGTCAAAACA CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

```

g793.pep
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKQGE GLELSLEDSL
201 YGEDGAIEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIIILSLD QRIOTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRNR
301 AVTDMIEPFS AIKPFVIAKA LDAGKTDLNE RLNTQPKYIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSARFGAEEM YDFYHELIG VPMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQ GK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFDVGAFTG
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYGGVVVA
551 GPPFKRIMGG SLNILGISPT KPLTAAAVKT PS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

```

m793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAAAC TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGTGCG CCGACGGAGT CCCTGTTTGC CGTGCCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAA GCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAAGCCT TGGGTTTGGA AAACCTTTGTA TTTGAAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCGTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CCGTCAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCGGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1275

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1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACCTCGGCAC
1101 AAGCAAACGT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCCGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGCGGGG TCGGCTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAC ACATCGCTAC
1551 CTTTATCCGT TTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGCT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTT
1701 CCGGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

```

m793.pep
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNLFKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPAAQ LERLSELVDV PVDVLRNKLE QKGKFSFIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYP MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRP RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKIG PVPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRRW RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSE
451 KQAVAPQGRK IFKESTAREV RNLMVSVTEP GGTGTAGAVD GFDVGARTGT
501 ARKFVNRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

	10	20	30	40	50	60
g793.pep	MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAIAVLFACLIARGLYLQTVTYNLFKEQ					
m793	MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNLFKEQ					
	10	20	30	40	50	60
g793.pep	GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPAAQLERLSELVDV					
	70	80	90	100	110	120
g793.pep	PVDVLRNKLEQKGKFSFIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLEQKGKFSFIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
g793.pep	FTDIDGKGQEGLELSLEDSLYGEDGAEVVLDRQGNIVDSLDSPRNKAPQNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEDGAEVVLDRQGNIVDSLDSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
g793.pep	QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
g793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKIGPSPVRDTHVYPSLDVRGIM					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKIGPSPVRDTHVYPSLDVRGIM					
	310	320	330	340	350	360
g793.pep	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS					
	370	380	390	400	410	420
g793.pep	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS					
	360	370	380	390	400	410

1276

```

          430      440      450      460      470      480
g793.pep    FGYGLQLSLLQLARAYTALTHDGVLLPLSFQKQAVAPQKRFKKESTAREVRNLMVSVTE
            |||||
m793        FGYGLQLSLLQLARAYTALTHDGVLLPLSFQKQAVAPQKRFKKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep    PGGTGTAGAVDGFVDGAKTGTARKFVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
            |||||
m793        PGGTGTAGAVDGFVDGAKTGTARKFVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep    AHGYYGGVVAGPPFFKIMGGSNLILGISPTKPLTAAAVKTPSX
            |||||
m793        AHGYYGGVVAGPPFFKIMGGSNLILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCCGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAACA TTGCCGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTGG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGAATCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGC CGGTGCAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCGTAACCCG ATATGATCGA ACCCGTTTCG GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAATCG TCTGCGCGTT TCGGTGCGGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCTATCG AACAGGCGAC
1251 GATGCTTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCGGCA AGGCAAACGC ATATCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCAACCG
1451 GTACGGCGGG TGCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGGCGAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGTTATT ACGGCGCGCT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCAGCCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYP MGNLFHVIG FTDIDGRQGE GLELSLEDSL
201 HGEDGAEEVL RDRQGNIVDS LDSRNKAPK NGKDIILSLD QRIQTLYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFEHELIGIV RMHSGFPGET
401 AGLLRNRRR RPTEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSE
451 KQAVAPQGRK IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIAITFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFFKIMGGS LNILGISPTK PLTAAAVKTP S*

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a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKKEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLESLSDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLESLSDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAAGTGVVLDARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAAGTGVVLDARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALHDGVLLPVSFQKQAVAPQGGKRIFKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALHDGVLLPVSFQKQAVAPQGGKRIFKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	550	560	570	580		
	HGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	HGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

1	gtgcgtttca	ATCATTTCAT	AATGGTAACG	ATTATTATAT	ATGTGATTTT
51	CCCTGCAAAC	AAGCCGGTCC	GCCGCCCGG	CGTCCCACT	TATCCGGCTT
101	TGCCTTATAA	TTGCTTTTTT	TATGTAACAG	ATTCACCTAT	GAATTTCCCC
151	AAAACAGCGG	CCTCCCTGCT	GCTGCTTCTC	GCCTCCCTCG	CCGCACACGC
201	GCTCGATACC	GGCCGCATTC	CGCAAAACGA	AATCGCTGTA	TATGTCCAAG
251	AGCTTGACAG	CGGAAAAGTC	ATCATTGACC	ACCGTGCCGG	CATACCCGTC
301	AATCCCGCGT	CCACGATGAA	GCTCGTTACC	GCGTTTGCCG	CCTTCAAAC
351	CTTCGGCAGC	AATTACCGCT	GGGCGACCGA	GTTTAAAGC	AACGGTACGG
401	TAAACGACGG	CACGCTTGAC	GGAAACCTGT	ATTGGGCGGG	CAGCGGCAGC
451	CCCGTTTCA	ATCAGGAAAA	CCTGCTTGCC	GTCCAACGCC	AGTTGCGCGA
501	CAAAGGCATC	CGCAATATCA	CGGGGCGCCT	GATGCTCGAC	CACAGCCTGT

1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTITG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAAATCC GACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGGCGCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGCGTCAA AAAACTGATG CGGCATCTT TTTGCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCTGCT TCCTCAAAC TCGGCGCGAC GGCAACTGC CCGCGTTTC
1101 CGAACAGCGC GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAAATG TTGGAACGG CTTATTTTACG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCGGCGCGC
1501 GACGCGTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1  VRENHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNF
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLT GNLWAGSGD
151 PVFNQENLLA VORQLRDRGI RNITGRMLD HSLWGEVSP DHFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAOTLAVAH SKPMKEILD MNKRSNLI
351 RSVFLKLGDD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGLTRNRF KQSGGLLRK
451 TGTLLNVRL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVAKNIISGG
501 DGWLDKILMC KERRA*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1  GTGCGTCTCA ATCATTTTCA TATGATAGCG ATTATTATAT ATGTGATTTT
51  CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCCTTATA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CTTCAAAAC
351 CTTGCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTC AATCAGGAAA CCTGCTTGAT GCTCAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCATATCA CGGGACACCT GATGCTCGAC CAGACCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTTC AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGGCGCCGA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCCGC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAACTGATG CGTGATCTT TTTGCGACAA
801 TAGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTGCT TCCTCAAAC TCGGCGCGAC GGCAACTGC CCGCGTTTC
1101 CGAACAGCGC GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 AAGCTTCCGA TTTGGTTTGG GAAAACGGTT CGGGCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAAATG TTGGAACGG CTTATTTTACG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACCTTTAC CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGCGC
1501 GATGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1  VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV

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1279

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AQKQLREQGI LNTIGHMLD HSLWGEVGSF DDFEADSGSP
201 FMTFPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLTRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

g794/m794 95.5% identity in 515 aa overlap

      10      20      30      40      50      60
g794.pep VRFNHFIMVTIIIVISIPANKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLLL
m794      VRLNHFIMIAIIIVISIPANKPARRHVSPTYPALPYNCFYVTDLPNMFPKTAASLLLLL
      10      20      30      40      50      60
g794.pep ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS
m794      ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
      70      80      90      100     110     120
g794.pep ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
m794      ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
      70      80      90      100     110     120
g794.pep NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRLRDKGIRNITGRMLD
m794      NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQQLREQGIILNITGHMLD
      130     140     150     160     170     180
g794.pep NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRLRDKGIRNITGRMLD
m794      NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQQLREQGIILNITGHMLD
      130     140     150     160     170     180
g794.pep HSLWGEVGSFDDFEADSGSPFMTFPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
m794      HSLWGEVGSFDDFEADSGSPFMTFPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
      190     200     210     220     230     240
g794.pep HSLWGEVGSFDDFEADSGSPFMTFPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
m794      HSLWGEVGSFDDFEADSGSPFMTFPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
      190     200     210     220     230     240
g794.pep QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
m794      QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
      250     260     270     280     290     300
g794.pep QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
m794      QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
      250     260     270     280     290     300
g794.pep NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
m794      NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
      310     320     330     340     350     360
g794.pep NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
m794      NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
      310     320     330     340     350     360
g794.pep GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA
      370     380     390     400     410     420
g794.pep GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA
      370     380     390     400     410     420
g794.pep QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
m794      QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
      430     440     450     460     470     480
g794.pep QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
m794      QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
      430     440     450     460     470     480
g794.pep AVSLLPDLNDFVAKNIISGGDGWLDKLMCKERRAX
m794      AVSLLPDLNDFVANNIISGGDGWLDKLMCKERRAX
      490     500     510
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

```
a794.seq
1  GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCTCAT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTCCGATTC CGAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC
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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGGCCGA TATTTTCGCC AAAACAAC TGAATAATAC CGCCTCCCAA
751 GGTGCGCTGCC CTTCGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGAAGCCTG
851 TCGGTGTCGG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CTTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGGCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAACCGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAATG TTGGAACGG CTTATTTTACG
1251 CCCGTTTGCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTATT GGTGGGCGCA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCGCG CCGGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```
1 VRLNHFIMIA IIIYVISPA KPARRHVSPT YPALPYNCFF YVTDLPNMF
51 KTAASLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLWAGSGD
151 PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVGSF DDFEADSGSP
201 FMTFPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGDD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLPLDLN FVANNIISGG
501 DGWLDKLMC KERRA*
```

a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIAIIIYVISPA	KPARRHVSPTYPALPYNCFF	YVTDLPNMF	KTAASLLLL		
m794	VRLNHFIMIAIIIYVISPA	KPARRHVSPTYPALPYNCFF	YVTDLPNMF	KTAASLLLL		
	70	80	90	100	110	120
a794.pep	ASLAHALDTGRIPONEIAV	YVQELDSGKVIIDHRSDVP	NPASTMKLVT	AFAAFKTFGS		
m794	ASLAHALDTGRIPONEIAV	YVQELDSGKVIIDHRSDVP	NPASTMKLVT	AFAAFKTFGS		
	130	140	150	160	170	180
a794.pep	NYRWATEFKSNGTVNDGTL	DGNLYWAGSGDPVFNQENLL	AQQLREQGIRNITGHLMLD			
m794	NYRWATEFKSNGTVNDGTL	DGNLYWAGSGDPVFNQENLL	AQQLREQGIRNITGHLMLD			
	190	200	210	220	230	240
a794.pep	HSLWGEVGSFDDFEADSGS	PFMTFPNPTMLSAGMVMVRAE	RNAADSTDILTDPPLPHIFA			
m794	HSLWGEVGSFDDFEADSGS	PFMTFPNPTMLSAGMVMVRAE	RNAAGSTDILTDPPLPHIFA			
	250	260	270	280	290	300
a794.pep	QNNLKITASQAACPSIKKLM	RASFSDNTLKLRGNIPESCL	GKPVGVRMFALDELIRQSFT			
m794	QNNLKITASQAACPSIKKLM	RASFSDNTLKLRGNIPESCL	GKPVGVRMFALDELIRQSFT			
	310	320	330	340	350	360
a794.pep	NHWLLGGGRISDGIGISDTP	EGAQTLAVAHSKPMKEILTD	MNKRSNLIARSVFLKLGDD			

g900.seq

g900.pcp

m900.seq

1 ATGCCGCTCTG AAACGCGGCA GCGGAGGTT CGACGGCAT CGGGTTTCATT
51 TCAACGGGCG GATGcGCACC GCATcG.TA CTTTGTCCAA TAATTGCGGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTGATTTG

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151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CCGCGTTGAT TTTCCGCCGC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATTCACAC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATTT TTGGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGTGTTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGGCGATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCC GTTTTCTGCA
701 TTTGCTGCA CCGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCCGTAT
951 CGAGTTTTG CGCCGCGCGG ACGGCGGGG GATGCGGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTGAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCGGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

```

m900.pep
  1 MPSETRQAEV RTASGSFORA DADRIXFVQ *FACFFTRFR RACLQNLFDL
 51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPR NGVAVGFGHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTAIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHRLRV
301 AFDDTVVIGE EEEGFGIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QOTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

```

m900/g900

      10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFORADADRIXFVQXFACFFTRFRACLQNLFDLRRVGGQ
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      MPSEMPSETWQAEVRTALGLFORADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ
          10      20      30      40      50      60

      60      70      80      90     100     110
m900.pep  LVVAFARFGEFGVDFFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEGFVDFKQWAFVGLFRL
          ||||| :||| ||||| :||| :||| ||||| :||| :||| ||||| :||| |||||
g900      CVVAFQAQFCQFGVDFFRRKFFRLAPSAVAGKHLRKFRFRRRRGEGFIDFKQRAVGLFRL
          70      80      90     100     110     120

      120     130     140     150     160     170
m900.pep  ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFDFVDFHFGQGEFPEA
          ||||| :||| ||||| :||| :||| ||||| :||| :||| ||||| :||| |||||
g900      ARLFHVGNDFVDRFLGFFVVFPRKNGIAGVFGHFASVQTDQEFDFVDFHFGQGEFLET
          130     140     150     160     170     180

      180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICL
          ||||| :||| ||||| :||| :||| ||||| :||| :||| ||||| :||| |||||
g900      VGEAAGNVARHFDVLDLVAPDGHFVGVEHQNVGSHQNRITEQTHFHTIGVFLPVFRIGL
          190     200     210     220     230     240

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	240	250	260	270	280	290
m900 . pep	HGGFVGMGAVHQ	TLGSDAGQNPVQ	FHHFGSVALAVE	GGALGVESAGKP	SGGNGLGGLVNH	
	:	:	:	:	:	:
g900	NGGFVGVGAVHQ	TLGGDAGQNPVQ	LHHFGNVALAVE	GGALGVESAGKP	SGGNGLGGLVNH	
	250	260	270	280	290	300
	300	310	320	330	340	350
m900 . pep	LRLVAFDDTVV	IGEEEEFGIEVL	RRLADGGADGAD	VVAQMRDAGGGY	AGQNSFFAHKNVL	
	:	:	:	:	:	:
g900	LLLVAFDNAV	VIGEEEEFGIGV	LRLADGGADGAD	VVAQMRGAGGGY	AGQNSFFAHKNVL	
	310	320	330	340	350	360
	360	370	380			
m900 . pep	AASMPSEREKDV	PIIPDLPTSSRQ	QTFPYX			
	:	:	:	:	:	:
g900	TAAMPSEREKDA	PIIPDLPTSSRQ	QTFPYX			
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900 . seq	(partial)
1	GAGGTCGGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51	CACGTACTTT GCCCAATAAT TCGCGTGCTT CTTTACGCGC TTTTTCGCGG
101	CCTGCCTGCA AAATCTCTTC GATTTCGCGA GGGTCGCGCG TCAGCTCGTT
151	GTAGCGTTCG CGCGGTTCCG CGAGTTCGGC GTTGATTTC CCGCCAAAA
201	GTTTTTTTGC CTCGCCCAA GCCAAGCCGT CGGCAAGCAT TTTCGTAAT
251	TCTGCCGTTT CAGACGCGT GGAGAAAGCT TTGTAGATT CAAACAGAGG
301	GCTTTCGTCG GGCTTCTTCG GCTCGCCCGG CTCCTTCATA TTGGTGATGA
351	TTTTGTGAC CGATTTTGG GTTTTTTGT CGTTTTCCCA AAGCGGAATG
401	GTGTTGCCGT AGGATTGGA CATTTTTCGT CCGTCCAAAC CAACCAAGAG
451	TTTCAGCTTT TCGTCGATT TCACTTCGGG CAGTGTGAAG AGTCCCGGA
501	AGCGGTGGTT GAAGCGGCCG GCAATATCGC GTGCCATTTC AACGTGTTGG
551	ATTTGGTCGC GACCGACTGG AACTTCATGG GCATTGAACA TGAGAATGTC
601	GGCAGTCATG AGGATAGGGT AGCTGTACAA ACCCATTTCC ACGCCGAAAT
651	CGGGGTCTTC CTGCCGTTT TCCGCATTG CCGTCCAGGC GGCTTTGTAG
701	GCGTGGCGC GGTTCATCAA ACCCTTGGCG GTGATGCAGG TCAGAATCCA
751	GTTCAATTCC ATCACTTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801	GCTCGGGGTC GAGTCCGCG GCAAGCCAAG TGGCGGCAAC GGCTTGGGTG
851	GATTGGTGAA TCATCTCCG CTCGTGGCAT TTGATGATAC CGTGGTAATC
901	GGCGAGGAAG AGGAAGGATT CGGTATCAGG GTTTTGCGCC GCGCGGACGG
951	CGGGGCGGAT AGCACCACG TAGTTGCCCA GATGCGGGAT GCCGGTGGTG
1001	GTTACGCCG TCAGAACTCG TTTTTTGCTC ATAAAAATGT CCTTGCAGCA
1051	TCAATGCCGT CTGAAAGGGA AAAAGATGCG CCGATTATAC CCGATTGGCC
1101	ACCTACATCC AGCCGACAAC AGACTTTTCC ATATTAA

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900 . pep	(partial)
1	EVRTALGLFQ RADTDRTYF AQ*FACFFTR FLRAQLQNLF DLRRVGGQLV
51	VAFAFGEFG VDFRRQKFFC LAPSQAVGKH FRKFCRFRRR GESFVDFKQR
101	AFVGLRLRLR LFHIGDDFVD RFLGFFVVFV KRNGVAVGFG HFASVQTNQE
151	FDVFVDHFG QCEEFPEAVV EAAGNIACHF NVLDLVATDW NFMGIEHENV
201	GSHEDRVAVQ THFHAIEGVF LPVERICLHG GFVGVGAVHQ TLGGDAGQNP
251	VQFHHFGNVA LTVEGGALGV ESAGKPSGGN GLGGLVNHLR LVAFD DTVVI
301	GEEEEFGIR VLRRADGGAD STDVVAQMRD AGGGYAGQNS FFAHKNVLAA
351	SMPSEREKDA PIIPDLPTS SRQQTFFPY*

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900 . pep	MPSETRQAEV	RTASGSFQRA	DADRIXYFVQ	XFACFFTRF	RRACQLQNL	FDLRRVGGQLV
	:	:	:	:	:	:
a900	EVRTALGLFQ	RADTDRTYF	FAQXFACFF	TRFLRAQLQ	NLFDLRRVGG	QLVVA
	10	20	30	40	50	
	70	80	90	100	110	120

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m900.pep	FARFGEFGVD	FRRQKFFG	FTPRQAVG	KHFRKFHR	FRRRGEGF	VD	FKQWAF	VGLFRL	LARLF
a900	FARFGEFGVD	FRRQKFFCL	APSQAVG	KHFRKF	FCRFRRR	GESF	VD	FKQRA	FVGLLRLARLF
	60	70	80	90	100	110			
m900.pep	HIGDDFVDR	FLGFFV	VFPKRNG	VAVGFG	HFAVQ	TQ	ED	VD	FIDFHF
a900	HIGDDFVDR	FLGFFV	VFPKRNG	VAVGFG	HFAVQ	TQ	ED	VD	FIDFHF
	120	130	140	150	160	170			
m900.pep	AGDVARH	FDVLDL	VAPDGH	FVGV	EHQNI	GSHQ	NR	ITEQ	THFHT
a900	AGNIACH	FNVL	DLVATD	WNFM	GIEH	ENVG	SH	EDR	VAVQ
	180	190	200	210	220	230			
m900.pep	VGMGAVH	QTLG	SDAG	QNPV	QFHH	FGS	VAL	AVE	GGAL
a900	VGVGAVH	QTLG	SDAG	QNPV	QFHH	FGN	VAL	TVE	GGAL
	240	250	260	270	280	290			
m900.pep	AFDDTV	VIGEE	EGFG	IEVL	RRAD	GGAD	GADV	VQA	MRD
a900	AFDDTV	VIGEE	EGFG	IEVL	RRAD	GGAD	STDV	VQA	MRD
	300	310	320	330	340	350			
m900.pep	PSEREK	DVPI	IPDL	PPTSS	RQQT	FPYX			
a900	PSEREK	DVPI	IPDL	PPTSS	RQQT	FPYX			
	360	370							

g901.seq not found yet
g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

m901.seq

1	ATGCCCGATT	TTTCGATGTC	CAATTTGGCC	GTTGCCTTTT	CCATCACATT
51	GGCTGCCGGT	TTGTTTACCG	TATTAKGyAG	TGGCTTGGTG	ATGTTTTC
101	AAACGCCCAA	TCCGCGTGTG	TTGTCGTTTG	GTTTGGCGTT	TGCCGCGGGT
151	GCGATGGTAT	ATGTTTCCCT	GACGGAGATT	TTCAGTAAGT	CCAGCGAGGC
201	GTTGCTGAA	ATTTATGATA	AAGACCACGC	GTTTGGCGCG	GCGACCATGG
251	CATTTTGGC	CGGATGGGC	GGCATTGCGC	TGATTGACCG	TCTGGTGCCG
301	AACCCGCATG	AAACTTTAGA	CGCGCAAGAC	CCGTCGTTTC	AAGAAAGCAA
351	ACGCCGCCAT	ATCGCGCGAG	TCGGCATGAT	GGCGGCGTTT	GCGATTACTG
401	CGCACAAATT	CCCCGAAGGC	TTGGCGACGT	TTTTTGCCAC	ATTGAAAAAT
451	CCAGCAGTCG	GGATGCCTTT	GGCCTTGGCG	ATTGCCATCC	ATAATATTCC
501	GGAGGGCATT	TCCATCGCCG	CGCCGGTTTA	TTTTGCCACC	GCGAGCCGTA
551	AGAAAACGGT	GTGGGCGTGT	CTGCTATCCG	GCTTGGCCGA	GCCGTTGGGG
601	GCGGCTTTGG	GCTATTTGGT	TTTGCAGCCG	TTTTTGTCGC	CTGCCGTGTT
651	TGGTTCCGTA	TTCCGCGTGA	TAGCCGCTGT	GATGGTGTTT	TTGGCGTTGG
701	ACGAGCTGnt	GCCGGCTGCC	AAACGCTATT	CAGACGGCCA	TGAAACCGTT
751	TACGGCCTGA	CAACGGGTAT	GGCGGTGATT	GCCGTCAGCC	TGTTATTGTT
801	CCATTTTTAA				

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

m901.pep

1	MPDFSMSNLA	VAFSITLAAG	LFTVLXSGLV	MFSKTPNPRV	LSFGLAFAGG
51	AMVYVSLTEI	FSKSSEAFAE	IYDKDHAFAA	ATMAFLAGMG	GIALIDRLVP

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101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV
 251 YGLTTGMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq
 1 ATGCCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCCTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTCCCA
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTG GTTTGGCATT TGCCGGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTCGGCGC GCGACCATGG
 251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACCCGCATG AAACCTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGCGCGTTT GCGATTACTG
 401 CGCACAAATT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
 451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATCC
 501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCCAC CGCAGCCGTA
 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGG
 601 GCGGCTTTGG GCTATTTGGT TTGCGAGCCG TTTTGTGCG CTGCCGTGTT
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTT TTGGCGTTGG
 701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAACCGTT
 751 TACGGCCTGA CAATGGGCAT GCGGTGATT GCCGTCAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep
 1 MPDFSMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP
 101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTMGMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

	10	20	30	40	50	60
m901.pep	MPDFSMSNLA VAFSITLAAG LFTVLXSGLMVFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
a901	MPDFSMSNLA VAFSITLAAG LFTVLGSLVMFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
	10	20	30	40	50	60
m901.pep	FSKSSEAFAEIYDKDHAFAAATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
a901	FSKSSEAFAEIYDKDHAFAAATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
	70	80	90	100	110	120
m901.pep	IARVGMMAFAITAHNFPEGLATFFATLEN PAVGMPLALAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAFAITAHNFPEGLATFFATLEN PAVGMPLALAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
m901.pep	RSRKTWACLLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVIAGVMVFLALDELXPAA					
a901	RSRKTWACLLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVIAGVMVFLALDELLPAA					
	190	200	210	220	230	240
m901.pep	KRYSDGHETVYGLTTGMAVIAVSLVLFHFX					
a901	KRYSDGHETVYGLTMGMAVIAVSLVLFHFX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCGG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTC
151 ACGCCGCGCC TGTTCCGCGT CGGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCCTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCAATG
251 GCGCGGATGT GGTTCAAAAT GGCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAG ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgCggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTTCAGAc ggCTTTTGGT CTCGGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TCGGTGcgCG CGcgcccggtg aacggcaaGg
551 gcggaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgctcgtc tgccaaccca AacggGTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCTGc
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTCTtgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCGGAG TCCGACGTTg taacgcgcg
801 catCCGCCAT CtggtcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCCCT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCga TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQN GGSFQCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAIF GDFGDGGQVL
201 IVVVTQTGF EGNQYARRLD HRLQNGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDLPE SDVVTTRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATT TGGCGGTAGG
51  CGCACGCCCA ACTGTGCGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTGCGCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GCGCATTTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGCGCGC GGTGTGTTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCGGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC GATGAGTTTC TAACGCGCTT
501 CGCCTTTGTA CATTTCGTA CCGGTGCGTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCCGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTGCTG GTCAGCATT CCGCACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTGCGTAA TGCCCGCCAT CGGcGCaAGT
1001 CGGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902.pep
 1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
 51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQQTQGRR
 101 QNTVFGIMFQ IAEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
 151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAAFGD FGDDGQVLMV
 201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
 251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
 301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDDGVVDK IAADVHNGSA
 351 FQKSTPLYIF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT CLFAVGHF				
g902	10	20	30	40	50
	MPSEPERRHGNTALPFPFAARPTVGFSFGKPKITGKCVLRRRIVQAVDFTPRLFAVGHF				
m902.pep	60	70	80	90	100
	VDVPAYVFACDAHTGGVAVKRVYGADVQNSGGAFCQTQGRRQNTVFGIMFQIAEPRPA				
g902	60	70	80	90	100
	ADVVPAYVFACDAHTDGLTIKRVHGAADVQNGGSAFCQTQGRRXNAVFGIMLQIAEKPRPA				
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVDPPDRDVQTAFGFGDEFVTRFAFVHLRTRASV				
g902	120	130	140	150	160
	LRAAPYHDAVGGGLFEDGGGFLRRSDVAVDPPGRDVQTAFGLGDEFVTRLAFVHLRARAPV				
m902.pep	180	190	200	210	220
	DGKGGDAAFGDGDDGQVLMVVVPTQTGFEGNGYACRTDDGFGQNGGNQRLVLHQRATGL				
g902	180	190	200	210	220
	NGKGGNAAFGDGDDGQVLIVVPTQTGFEGNGYARRLDHRLQNGGNQRLVLHQRATGL				
m902.pep	240	250	260	270	280
	DIADFFSGTAHVVDKLRPKADVVTGIRHLLRIASGNLHGNNAFIGKIAAVQGFSSIS				
g902	240	250	260	270	280
	DVAHFLGGAHIDVDLDPESDVVTRIRHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
m902.pep	300	310	320	330	340
	ERRVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLY				
g902	300	310	320	330	340
	ERRIAGQHFAHRPTCAKRPTAAEGFVGNARHRRKCDGVVDKITADVHNGPAFQKSAPLY				
m902.pep	360				
	IFX				
g902	360				
	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

1 TTGCACTTTC AAAGGATAAT CAAGTGTTC GAAGGCATT GGGCGGTAGG
 51 CGCAGCCCCA ACTGTCGGTT TTTTCGGCAA GTCTTCAAG ATACCTGCA

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```

101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAACACCG TGTCGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTC CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTGCGTG CGCGTGCGTC CGTGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAACG CCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGGC
1051 TTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

```

a902.pep
1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51 CLFAVGHEVD VPAYVFACDA HTGGVAVKRV HGSDEVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEEPRLALR AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGGNAALFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDDGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

```

          10      20      30      40      50      60
m902.pep  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHEVD
          |||
a902      LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHEVD
          10      20      30      40      50      60

          70      80      90      100     110     120
m902.pep  VPAYVFACDAHTGGVAVKRVYGVADVQNSGGAFQCQTQGRRQNTVFGIMFQIAEEPRLALR
          |||
a902      VPAYVFACDAHTGGVAVKRVHGSDEVVQNSGGTFCQTQGRRXNTVFGVMFQIAEEPRLALR
          70      80      90      100     110     120

          130     140     150     160     170     180
m902.pep  AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG
          |||
a902      AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRTRASVDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m902.pep  KGGDAALFGDFGDDGQVLMVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI
          |||
a902      KGGNAALFGDFGDDGQVLMVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI
          190     200     210     220     230     240

          250     260     270     280     290     300
m902.pep  ADFFSGTAHVVDVKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER
          |||
a902      ADFFSGTAHVVDVKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER
          250     260     270     280     290     300

          310     320     330     340     350     360
m902.pep  RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF

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|||||
a902   RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
              310      320      330      340      350      360

m902.pep   X
            |
a902       X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51  TCCTATTTCT GAGGTGGAAAT TGGTGGGTGA aGaaacggct aaATTCGGgt
101 tTGCCTcaaa ccaTGCCTTG tgccAAACAC ATTTTgtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAatcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAaccctga tgccggGCTA TCtgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATGcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTGGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGCGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAATC ACTGTACAAC GCGTAAAAAC CACAGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATTT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACCCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGA AAAAGCC cgaatatatt cAGACGAAGA Aatgggtaac
1551 999gtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51  LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAFAQ NKFPTRSNL LNLRLDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKS YIDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTFFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVVRGFDGE MSLPAERGWY WRNDLSWQFK
451 PGHQLYLGLAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIPT
501 GRALKKPEYF QTKKWTGFFQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTTAACTG ATGCAAATGT
51  CCGTTTCGAG CAACCATTTG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AACACCCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

```



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151 CGCAAATTTT CTTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTG GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCAATC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TGCGTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTCAGT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCTTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
701 TTTCAATATG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAG CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTTC CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRVEEKRDG KSAEGSISAF NNFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNGKQ
301 YQSSLAERM LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRLAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGDI LPGTSRMKII
401 TASLDAAAPF XLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

              10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
              |:::| |:::| |:::| |:::|
g903      MATQVGGANSDEASPCFP ISEVELVGEETAKFRFALNHA
              10      20      30

              70      80      90     100     110     120
m903.pep  MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
              :| | | | | : : : : : | | | | : : | : : | :
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKQLTLMPGYLR
              40      50      60      70      80      90

```

1291

	130	140	150	160	170	180
m903 . pep	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLENLRLPSVKTDIQIIPSE					
g903	SIRIDRSNDDQTHAGRIAAFQNKFPTRSNDDLNLRLDLEQGLENLKCLPTAEADLQIVPVE					
	100	110	120	130	140	150
	190	200	210	220	230	
m903 . pep	EE-GKSDLQIKWQONK-PIRFSIGIDDAGGKTGKYQGNVALSFDNPLGLSDLFVVSYGR					
g903	REPNQSDVVQWRXLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMFVYNYGR					
	160	170	180	190	200	210
	240	250	260	270	280	290
m903 . pep	GLAHKTDLTATGTETESGSRYSVHYSVPVKWLFSFNHNGHRYHEATEGYSVNYDYNG					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNGYRYHQAVSGLSEVYDYNG					
	220	230	240	250	260	270
	300	310	320	330	340	350
m903 . pep	KQYQSSLAERMLWRNRLHKTSGVMKWLTRQTYKYIDDAEIEVQRRRSAGWEAELRHRA					
g903	KSYNTDFGNRLLYRDAKRKTYLSVKLWTRTKSYIDDAELTVQRRKTTGWLAELSHKGY					
	280	290	300	310	320	330
	360	370	380	390	400	410
m903 . pep	LNRWQLDGKLSYKRGTGMRQSMPEENGDDILPGTSRMKIIITASLDAAPFXLGKQOFF					
g903	IGRSTADFKLKYKHGTGMKDALARPEEAFGE---GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390
	420	430	440	450	460	470
m903 . pep	YATAIQAWNKTPPLVAQDKLSIGSRYTVRFGDGEQSLFGERGFYQNTLTWYFHPNHQFY					
g903	YDTSVHAQWNKTPPLTSQDKLAIGGHHTVRFGDGEMSLPAERGWWYWRNDLSWQFKPGHQLY					
	400	410	420	430	440	450
	480	490	500	510	520	530
m903 . pep	LGADYGRVSGESAQYVSGKQLMGAVVGFGRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
g903	LGADVGHVSGQSAKWLSGQTLAIGTIRGQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
	540					
m903 . pep	YGFNLNYSFX					
g903	TGFQVGYSEFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903 . seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	AACTGGGATG	TGTTTAGGTT	CCAATAATT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATT	GGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATT	AATAACAAAT	TCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCGCGATGT	AGAGCAGGGC	TTGGAAGAAC	TGCGTCGTTT
501	CCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAAGAAGGCA
551	AAAGCGATT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTCAGT

1292

```
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 ATTCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGAT TGGATGCAGC GGCCCGGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTGTAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```
1 MQRQQHIDAE LLTDANVRFE QPLEKNYYVL SEDETPCTRV NYISLDDKTA
51 RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NKNKFLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERM LWRNRFHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGGGT IPGTSRMKII
401 TAGLDAAAF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*
```

m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE LLTDANVRFE QPLEKNYYVL SEDETPCTRV NYISLDDKTVRKFSFLPSVL					
a903	MQRQQHIDAE LLTDANVRFE QPLEKNYYVL SEDETPCTRV NYISLDDKTARKFSFLPSVL					
	10	20	30	40	50	60
m903.pep	MKETAFKTMCLGSNNLSRLQKAAQQILIVRGYLTSAIIQPQNMDSGILKLRVSAGEIG					
a903	MKETAFKTMCLGSNNLSRLQKAAQQILIVRGYLTSAIIQPQNMDSGILKLRVSAGEIG					
	70	80	90	100	110	120
m903.pep	DIRYEEKRDGKSAEGSISAFNNKFLYRNKILNLRDVEQGLNLRRLPSVKTDIQUIPSE					
a903	DIRYEEKRDGKSAEGSISAFNNKFLYRNKILNLRDVEQGLNLRRLPSVKTDIQUIPSE					
	130	140	150	160	170	180
m903.pep	EEGKSDLQIKWQONKPIRFSIGIDDAGGKTTGKYQGNVALSFDNPLGLSDLFYVSYGRGL					
a903	EEGKSDLQIKWQONKPIRFSIGIDDAGGKTTGKYQGNVALSFDNPLGLSDLFYVSYGRGL					
	190	200	210	220	230	240
m903.pep	AHKTDLTDATGTETESGSRSSVHYSVPVKKWLFSFNHNGHRYHEATEGYSVNYDYNKGQ					
a903	VHKTDLTDATGTETESGSRSSVHYSVPVKKWLFSFNHNGHRYHEATEGYSVNYDYNKGQ					

1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKTSVGMKWLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKTSVGMKWLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTMGRQSMPEENGDDILPGTSRMKIITASLDAAPFXLGKQOFFYA					
a903	RWQLDGKLSYKRGTMGRQSMPEENGDDILPGTSRMKIITASLDAAPFXLGKQOFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYQNTLTWYFHPNHQFYLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTGCGGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCGCCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CCGTCGGGAA
451 CCGGCCCCGA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTGTTCAA CACGCGggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCCGCA
951 TGTGTAAGG CAGGATCAGC GGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAAGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGCCG CCTTGAAGC GCACgacGct
1201 gCCGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRFFAV GAGGDDGDRR AADFFNPFI CFIQRQCVV AFHADSRFAP

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1294

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51 AGHGFVNRF A GFHRIARTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNIQIH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNNRR NARRDFFDNR HHVFRFNRSG
251 VMQVLELDV IGKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF AGLVERDVVR QDQRAGRRDF QTAFDVVFHAC RVQLVDFAAQ
351 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYNYIFSHS HITRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

```

m904.seq
1 ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51 CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTCACACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAATT CCGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC TCGCGCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGC AATGCGGGC
701 GCGACTTTTT CGATAACCGC CATCAGCTCT TCCGCTTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTTCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTC AAGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTGCCGCG GCG.ATcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GCGTTCGGGG GAGACGACAA CGCCGAACC GATGAAGCAG TCCAAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AATGGTTTTT TTTGCGCGCG
1151 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACCaCGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTAsT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

```

m904.pep
1 MMQHNRFVSFV GAGGDDGDRR AADFFNPFI CFGVFGQCAV VLHAESGFAP
51 AGHGFVNRLA GFHRIARTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAPCQTY AYFVEQFGRE
151 RARTDARGIG FDDAQNIQIH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFQKQ FFAVFVFLVQ HAGHVGNNRR NARRDFFDNR HHVFRFNRSLG
251 IVQMLQLDIV IGKDGIOFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAAXIF AGLVERDVVR QDQRAGRRDF QTAFDVVFHAC RVQLVDFAAQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMAR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXNYIFSHS HITRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

```

m904/g904
10 20 30 40 50 60
m904.pep MMQHNRFVSFV GAGGDDGDRR AADFFNPFI CFGVFGQCAV VLHAESGFAP AGHGFVNRLA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g904 MMQHNRFVAV GAGGDDGDRR AADFFNPFI CFI GIGRQC VVAFHADS RFAPAGHGFVNRF
10 20 30 40 50 60
70 80 90 100 110 120

```

1295

m904 . pep	GFHRIGTARQDVGF	AAVQGFIADADIDG	FNNAVHYIEFSNTH	TGNAVDLDGAFQGG	GGIKPA
g904	GFHRIR	TARQDVGF	AAAWQFVADADIDG	FNNAVHYIEFGNAHT	TGNAVDLDGAFQGGGIKPA
	70	80	90	100	110 120
m904 . pep	AAACASGYRTEFVS	AFCQTYAYFVEQFGR	ERARTDARGIGFDDA	QNIIOHLRTYARACRS	
g904	AAARAAGYRTEFVS	ALRQTCAFYVEQFGR	ERARTDARGIGFDDA	QNIIOHLRTYARACRS	
	130	140	150	160	170 180
m904 . pep	CARQTVGRGNEGISA	VVDVQRTLRAFQKQFF	AVFVFLVQHAGHVGN	HRNRARRDFFDNR	
g904	RAGETVGRGNEGISA	VVDVQRTLRAFQKQFF	AVFVFFVQHAGHVGN	HRNRARRDFFDNR	
	190	200	210	220	230 240
m904 . pep	HHVFRFNRLGIVQML	QLDIVIGKDGIOFFTQ	FXRMQOIGGANGAACH	FFVGRADAAAGR	
g904	HHVFRFNRSQVMQVLE	LDVVIGKDGIOFFTQ	FXRMQOIGGANGAACH	FFVGRADAAAGR	
	250	260	270	280	290 300
m904 . pep	ADFAFAARI	FAGLVERDVVRQDQ	RAGRRDFQTA	FDVFHACRVQLVDF	FAQQGGFGDDNART
g904	ADFAFAARCF	FAGLVERDVVRQDQ	RAGRRDFQTA	FDVFHACRVQLVDF	FAQQGGFGGNDNART
	310	320	330	340	350 360
m904 . pep	DEAVQTFMQDAARNQ	AQNGFFAADNOGMARI	VAALEAHHAAGFFRQ	PVNDFTFTLVAPLC	
g904	DEAIQSFVQDTARNQ	AQNGFFAADNOGMARI	VAALEAHDAAGFFRQ	PVNDFTFTLVAPLC	
	370	380	390	400	410 420
m904 . pep	ADXYNIFSHSHITYRYX				
g904	ADYYNIFSHSHITYRYX				
	430				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTCGCTCCA
151	ACCGGCATG	GTTTCGTAAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	CCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTGGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACCGACC	GCAGCGGCGT	GCGGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGCGCT	ACGCCCAGCG	CTGCCGAAGC	CGCGCCGGCG
551	AGGCAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCCG	TTTTTGTTTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGCGGT	AATGCGCGGC
701	GCGACTTTTT	CGATAACCGC	CATCAGCTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCTG
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

1296

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951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATT TCCTCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

```

a904.pep
1  MMQHNRRFAV GAGGDDGDRR TADFFNPFQI CFGIGR*CVV AFHAESGFAP
51  TGHGFVNRLA GFYRIRAAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVLDLG AFQGGGKPA AAACASGYRT EFVS AFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQQ FFAVFVFFVQ HAGHVGNNRR NARRDFFDNR HHVFRFHRLG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQAGRRDF QTAFDVFHAC RVQLVDFACQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

m904.pep	10	20	30	40	50	60
	MMQHNRRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA					
a904	MMQHNRRFFAVGAGGDDGDRRTADFFNPFQICFGIGRXCVVAFHAESGFAPTGHGFVNRLA					
	10	20	30	40	50	60
m904.pep	70	80	90	100	110	120
	GFHRIGTARQDVGFVAVGQFIADADIDGFNAVHYIEFSNTHTGNVLDLDAFQGGGKPA					
a904	GFYRIRAAARQDVGFVAVGQFVADADIDGFNAVHYIEFGNTHTGNVLDLDAFQGGGKPA					
	70	80	90	100	110	120
m904.pep	130	140	150	160	170	180
	AAACASGYRTEFVS AFCQTYAYFVEQFGRERARTDARGIGFDDAQNIQHLRTYARACRS					
a904	AAACASGYRTEFVS AFCQTCSD FVEQFGRERARTDARGIGFDDAQNIQHLRAYARACRS					
	130	140	150	160	170	180
m904.pep	190	200	210	220	230	240
	CARQTVGRGNEGISAVVDVQORTLRAFQQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR					
a904	RAGEAVGRSNEGVS AVVDVQORTLRAFQQFFAVFVFFVQHAGHVGNNRRNARRDFFDNR					
	190	200	210	220	230	240
m904.pep	250	260	270	280	290	300
	HHVFRFNRLGIVQMLQLDIVIGKDGIQFFTQFXRMQQIGGANGAACHFVFVGRADAAAGR					
a904	HHVFRFHRLGIVQMLQLDVVISKDGIOFFTQFFRMQQIGGANGAACHFVFVGRADAAAGR					
	250	260	270	280	290	300
m904.pep	310	320	330	340	350	360
	ADFAFAAXIFAGLVERDVVRQDQAGRRDFQTAFDVFHACRVQLVDFACQGGFGGDDNART					
a904	ADFAFAARCFSGLVERDVIRQDQAGRRDFQTAFDVFHACRVQLVDFACQGGFGGDDNART					
	310	320	330	340	350	360
m904.pep	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHASGFFRQPVNDFTFTLVAPLC					
	370	380	390	400	410	420

430

1297

```

m904.pep    ADXYNIFSHSHITYRYX
            || ||||| ||||| |||
a904        ADYYNIFSHSHITXRYX
            430

```

g906.seq not found yet
g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51  GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCCT
51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTGACa ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGA AGATTCTGTC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEDEGER RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51  GTTGTGTGCC GCCGGTGCCT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGA AGGTTCTGTC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTkTGG AAAAActACA TCGGCAAAACC GGCGCACAAAC
451 CTGTTGACa TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLSPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

```


Homology with a predicted ORF from *N. gonorrhoeae*

g907/m907

a907 . seq

a907.pap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDDASVMRSSVGSVNPRL					
	:		:			:
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQREETLADDDASVMRSSVGSINPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
a907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m907.pep	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
a907	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180
	190	200				
m907.pep	ARFNGSLGSNKYPNAVLGAWNRNRQWRX					
a907	ARFNGSLGSNKYPNAVLGAWNRNRQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTACGATG ACTGATTTAT
151 CAAAACGTC CGCATT TAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA AC GCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaaa cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIVYTD CY RSYDVLDVSE FSHFSAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATT TGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA AC GCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATAC GGATTGTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIFYTD CY RSYDVLDVRE FSHFSAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g908/m908						
g908.pep	MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRXLIYQNGPHLEMF D					

1300

m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAAYFHRRLRLLIYQNSPHLEMPD
	10 20 30 40 50 60
g908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLFPPIIREQVK
m908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLFPPIIREQVK
	70 80 90 100 110 120
g908.pep	PDSIVYTD CYRSYDVLDVREFSHFSFAETSFSYSQSHTCRRTTKPYX
m908	PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYSQSHTCRRTTKPYX
	130 140 150 160

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

a908.seq

```

1 ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAATAAAC TCATTGAGCT
51 ATTTGTGCGCA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGA AATGTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GCGCGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

a908.pep

```

1 MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNNTAA YFHRRLRLLI Y
51 QNSPHLEMPD GEVEADESYF GGQRKGKGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPPIIREQVK PDSIVYTD CY RSYDVLDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

m908/a908 98.2% identity in 166 aa overlap

m908.pep	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAAYFHRRLRLLIYQNSPHLEMPD
a908	MRKSRLSQYKQXKLIELFVAGVTARTAAELVGVNKNNTAAAYFHRRLRLLIYQNSPHLEMPD
	10 20 30 40 50 60
m908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLFPPIIREQVK
a908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLFPPIIREQVK
	70 80 90 100 110 120
m908.pep	PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYSQSHTCRRTTKPYX
a908	PDSIVYTD CYRSYDVLDVREFSHFSFAETSFSYSQSHTCRRTTKPYX
	130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

g909.seq (partial)

```

1 atgcgtaaaa ccgtacttat cCTgaccatc tccgcccggc tttgtcggg
51 ctgcacatgG gaaacttatac aagacggcag cggcaaaacc gccgtccgtg
101 caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```

1301

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
 201 caaccaaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
 251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
 301 acgggggagg ggaagcgatc ggcgagg..

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
 51 KKVDCDEYGG ERRAVLNRQK RGKPATRRAA TLGKPSFRAR DGGGRVNRAE
 101 TGEKRSAR..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTTGTGGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACCC
 201 CAATCAAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AACCAAAGTT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

1 MRKTFLEFLTA AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQ TGNNADEEHRQ HWQKPKFQNR *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		: : : : : : :	: : : : : : :	: : : :	: : :	: : : :
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	KKVDCDEYGG
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQ	TGNNADEEHRQ	HWQKPKFQNRX			
	: : :	: :	: : :			
g909	ERRAVLRNQ	KRGKPATRRA	ATLGKPSFRAR	DGGGRVNRAE	TGEKRSAR	
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTTGTGGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACCC
 201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AGCCCAAATT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

1 MRKTFLEFLMT AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQ TGNNADEEHRQ HWQKPKFQNR *

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		: : : : : : :	: : : : : : :	: : : :	: : :	: : : :
a909	MRKTFLEFLMT	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
	10	20	30	40	50	60

1302

```

              70      80      90
m909.pep    ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX
            |||
a909        ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51 ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRKA VKMLEQRGYQ
51 VYDVDADDYW GKPVEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51 ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATGCG GGTAAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLAAAAFAG DSAERQIYGD PHFEQNRKA VKMLEQRGYQ
51 VYDVDADDHW GKPVEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

```

g910/m910
              10      20      30      40      50      60
g910.pep    MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRKAVKMLEQRGYQVYDVDADDYW
            |||
m910        MKKLLLAADVSLAAAAFAGDSAERQIYGDPHFEQNRKAVKMLEQRGYQVYDVDADDHW
              10      20      30      40      50      60

              70      80      90
g910.pep    GKPVEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
            |||
m910        GKPVEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51 ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATGCG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTG TCTTACCCCG
251 ACCTGAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910.pep

```

1303

1 MKKLLLVAVV SLAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLAADVSLSAAAFAGDSAERQIYGDYPHFEQNRTKAVKMLEQRGYQVYDVDADDDHW					
	: : : : : :					
a910	MKKLLLVAVVSLAATAFAGDSAERQIYGDYPYFEQNRTKAVKMLEQRGYQVHDVDADDDHW					
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	: : : : :					
a910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq
1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG
51 CGCGGCGGCG GTTGCCTTTC TCGCTTTCG CGTGGCGGGC GCGCGGCGGT
101 TCGGCGGTTC GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCGTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTTGATT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNAEGGNAE KAAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq
1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
51 CGCGGCGGCG GTTGCCTTTC TCGCTTTCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCGTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10	20	30	40	50	60
----	----	----	----	----	----

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAFVK
|||||
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAFVK
              10      20      30      40      50      60

              70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
|||||
m911      SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
|||||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGA CTGTTTCG TCCTGATTGG
51  CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATT TCGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT
401 CTGCAATGGT TCTGGAAAC CTTATCGGCA AATTCATGAC GAGTTTGGC
451 GAGAAAAATG CCGACGGCGG CAATGCCGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFFGGSDKT YAVYADFGDI
51  GGLKVNAFVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAFVK
|||||
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAFVK
              10      20      30      40      50      60

              70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
|||||
a911      SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
|||||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTGAGCAT
51  CGGCATGGCA TTTGCCCTCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

1305

```

151 CGCCCAAAAG CCGAAGCCTA TCGGTTCCCG TATTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG TACCGCGTCC GACGCGCAAA
251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTCAA AACGCGACC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAGGGCGGCA AGGAAATCGT CGTCCGTGCC GAAGTCGGCA
401 TCCCCGGTCA GAAGCCCGTC AATATGGACT TTACCACCTA CCAAAGCGGC
451 GGCAAATACC GTACCTACAA CGTCGCCATC GAAGGCACGA GCCTGGTTAC
501 CGTGTAACGC AACCAATTG GCGAAATCAT CAAAGCCAAA GGCATCGACG
551 GGCTGATTGC CGAGTTGAAA GCCAAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

```

g912.pep
1 VKKSSFISAL GIGILSIGMA FASPADAVGQ IRONATQVLT ILKSGDAASA
51 RPKAEAYAVP YFDFQRM TAL AVGNPWR TAS DAQKQALAKE FOTLLIRTYS
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKRYTYNVAI EGTSLVTVYR NQFGEI IKAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

```

m912.seq
1 ATGAAAAAAT CCTCCCTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51 CCGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAGCCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA ACGGCGATGC CAACACCGCT
151 CGCCAAAAAG CCGAAGCCTA TCGGATTCCC TATTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTAACGC AACCAATTG GCGAAATTAT CAAAGCGAAA GCGTGGACG
551 GACTGATTGC CGAGTTGAAA GCCAAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

```

m912.pep
1 MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRONATQVLS ILKNGDANTA
51 RQKAEAYAIP YFDFQRM TAL AVGNPWR TAS DAQKQALAKE FOTLLIRTYS
101 GTMLKLNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKRYTYNVAI EGASLVTVYR NQFGEI IKAK GVDGLIAELK AKNGGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

```

g912/m912
          10      20      30      40      50      60
g912.pep  VKKSSFISALGIGILSIGMAFASPADAVGQIRONATQVLTILKSGDAASARPKAEAYAVP
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m912       MKKSSLISALGIGILSIGMAFAAPADAVSQIRONATQVLSILKNGDANTARQKAEAYAIP
          10      20      30      40      50      60

          70      80      90     100     110     120
g912.pep  YFDFQRM TALAVGNPWR TASDAQKQALAKEFOTLLIRTYS GTMLKFKNATVNVKDNPIVN
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m912       YFDFQRM TALAVGNPWR TASDAQKQALAKEFOTLLIRTYS GTMLKLNANVNVKDNPIVN
          70      80      90     100     110     120

          130     140     150     160     170     180
g912.pep  KGGKEIVVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTVYR NQFGEI IKAK
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m912       KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTVYR NQFGEI IKAK
          130     140     150     160     170     180

          190
g912.pep  GIDGLIAELKAKNGGKX

```


1306

```

      |:|||||||||
m912  GVDGLIAELKAKNGGKX
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

```

a912.seq
1   ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51  CGGCATGGCA TTTGCCGCC CTGCCGACGC GGTAAACCAA ATCCGTCAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TGCATTCCC TATTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTGGCG CACCGGTCC GACGCGCAA
251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAATTAAA AACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGCGGCA AAGAAATCAT CGTCCGCCGC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGATCCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

```

a912.pep
1   MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
51  RQKAEAYAIP YDFQRM TAL AVGNPWR TAS DAQKQALAKE FQTLIRTYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEI I KAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

```

m912.pep      10      20      30      40      50      60
MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
a912          10      20      30      40      50      60
MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP

m912.pep      70      80      90      100     110     120
YDFQRM TALAVGNPWR TASDAQKQALAKEFQTLIRTYS GTMLKLKNANVNVKDNPIVN
|||||||||||||||||||||||||||||||||||||||||||||||||||||
a912          70      80      90      100     110     120
YDFQRM TALAVGNPWR TASDAQKQALAKEFQTLIRTYS GTMLKLKNANVNVKDNPIVN

m912.pep     130     140     150     160     170     180
KGGKEIIVRAE VGVPGQKPV NMDFTTYQSGGKYRTYNVAIEGASLVTYR NQFGEI I KAK
|||||||||||||||||||||||||||||||||||||||||||||||||||||
a912         130     140     150     160     170     180
KGGKEIIVRAE VGVPGQKPV NMDFTTYQSGGKYRTYNVAIEGASLVTYR NQFGEI I KAK

m912.pep      190
GVDGLIAELKAKNGGKX
|||||||||||||:|
a912          190
GVDGLIAELKAKNGSKX
190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

```

g913.seq
1   atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTG GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTC AAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTAAACAACC TCGCGACGT GGTCA GTTTC GGCAGCAATA
251 TCTTGC GTT GGAc at CAAA cgcgcAAGcg aAGACctcgT CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGgcgGGCTC ATTGATATTG CCGGcgcGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TTCGTgttgc CCGTcttagg cccgtccacc

```

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```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcggttttc cataccctctg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtag gcgcgaaggc ctctcgatt tgaccgacag Tctggacgaa
601 gccgcatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

```

g913.pep
1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVTP KPVVAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWGTT AAAAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAEE
251 PAVHEDSVSE TQEAAGEAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

```

m913.seq
1 ATGAAAAAAA CCGCCTATGC CTCCTCCTG CTGATCGGGT TCGCTTCCGC
51 CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTGCGCCCT
151 GCGCGCGCGG GCTACCGCAA AGTTGCGCGG AAACCCGTCC GCGCGGCGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTGAGCTTC GGCAGCAATA
251 TCTTGCCTTT GGACATCAA CCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTCGGTTT GGGCGGGCTT ATCGACATCG CCGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
401 GATGAAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

```

m913.pep
1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51 AARGYRKVAP KPVVAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGT AVSAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

g913/m913

```

          10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVTP
          |||||:|||||
m913      MKKTAYAFLLLLIGFASAPAF AETRPADPYE GYNRAVFKFNDQADRYIFAPAARGYRKVAP
          |||||:|||||
          10      20      30      40      50      60

          70      80      90     100     110     120
g913.pep  KPVVAGVSNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||||:|||||
m913      KPVVAGVSNFFNNLCDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGIP
          |||||:|||||
          70      80      90     100     110     120

```

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	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWNKSNYFVLPVLPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWNKSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGGCCGA CCCTATGAA GGCTACAACC
101 GCGCCGTTT CAAATTC AAC GACCAAGCCG ACCGCTACAT TTTGCGCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTAACAACC TGTGCGACGT GGTGAGCTTC GGCAGCAATA
251 TCTTGCCTT AGACATCAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGA AAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TCGCGCGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51  AARGYRKVAP KPVRAVGSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWNKSNY FVLPVLPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*
  
```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVRAVGSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGL IDIAGAGGIP					
a913	KPVRAVGSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGL IDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWNKSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT					
a913	DNKNTLGDTFASWGWNKSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAEAEETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAEAEETQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacggttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCTG
451 taggctTCGA CGATTTTGTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTCAA TCCCATTG ATGTTTTTGG GCAGGTegaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTGTG TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGA GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTTCGTAGG CTTTCGACGAT TTTTTCGACC AAAGGATGCC GGACAACGTC
501 TTGCGCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTGG
601 CTGGTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGGTCAG
651 GAACATTTTC ATTTGTTCCG GCGTGGTGTT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

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151 DSXASTIFCT KGCRTTSSPV KWKYSPSTL CSFSRASFPD LMFGLRSIW
 201 LVSPVMTAFA PKPMRVNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLES GGNTVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLES GGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRC RKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRC RKFDXCIGWTDKETDTD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDFPCIGFQTALCQSCSADSXASTIFCTRG CRTTSSPVKWKYSPATP					
m914	TELGFRLCFSLPDFPCIGFQTALCQSCSADSXASTIFCTKGC RTTSSPVKWKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGGG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGCGGTG CAACCGCGAA ACTTCGGCAA TGTTTTCGCA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTT TGCCGATTTC
451 TAGGCTTCGA CGATTTTTCG CACCAAAGGA TGCCGGACAA CGTCTTCGCC
501 GGTAAGGTG TGGAATACA GCCCTTCCAC GCCGTGCAGT TTCTCAGCGG
551 CATCTTTTAA TCCCGATTG ATGTTTTCG GCAGGTGCAT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGG TGTTTTCGCG TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAG CGTCCTGCCG CGCATATAG
```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPADFAD RIGDLEARLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEEA
101 IRCRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFPDNL MFLGRSIWLV
201 SPVMTAFAPK PMRVNIFIC SGVVFCASSR MMYAPLSVLP RI*
```

m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
a914	MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLESGSNTVKIDLFSGNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGRICFSLPDPFCIGFQTALEQCSCSADSXSASTIFCTKGCRRTSSPVKWKYSPSTL					
a914	TELGRICFSLPDPFCIGFQTALEQCSCSADSXSASTIFCTKGCRRTSSPVKWKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

1	ATGAAGAAAA	CCCTGTTGGC	AATTGTTGCC	gtTTTCGCCT	TAAGTGCCTG
51	CCGGCaggcg	gaAGaggcac	cgccgCCTTT	ACCCCGGCAG	AtTAGCGacc
101	gttcggtcgg	aCACTAttgC	Agtatgaacc	tgaccgaaca	caacggcccc
151	aaagcccaga	tttttttgaa	cGGCAAACCC	GATCAGCCCG	TTTGGTTCTC
201	CACCGTcaag	cagatgttcg	GCTATACCAA	GCTGCCCGAA	GAGCCCAAAG
251	GCATCCGCGT	GATTTACGTT	ACCGATATGG	GCAATGTTAC	CGATTGGACG
301	AATCCTAATG	CCGACACGGA	GTGGATAGAT	GCGAAAAAAG	CCTTTTACGT
351	CATCGACAGC	GGCTTTATCG	GCGGTATGGG	CGCGGAAGAC	GCGCTGCCGT
401	TCGGCAACAA	GGAGCAGGCT	GAAAAATTG	CAAAGGATAA	AGGCGGCAAG
451	GTCGTCGGTT	TTGACGATAT	GCCCGATGCT	TACATTTTCA	AGTAA

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

1	MKKTLAIVA	VFALSACRQA	EEAPPPLPRQ	ISDRSVGHYC	SMNLTEHNGP
51	KAQIFLNGKP	DQPVWFSTVK	QMFGYTKLPE	EPKGIRVIYV	TDMGNVTDWT
101	NPNADTEWID	AKKAFYVIDS	GFIGGMAED	ALPFGNKEQA	EKFAKDGGK
151	VVGFDMPDA	YIFK*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

1	ATGAATAAAA	CCCTGTTGGC	AATTGTTGCC	GTTTCGCCT	TAAGTGC.tG
51	CCGGCAGGCG	GAAGAGGGAC	CGCCGCCTTT	ACCcCGGCAG	ATTAGCGACC
101	GTTCCGTCGG	AACTATTGAC	AGTATGAACC	TGACCGAACA	CAACGGCCCC
151	AAAGCCCAAG	TTTCTTGAA	CGGCAAACCC	GATCAGCCCG	TtTGGTTCTC
201	CACCATCAAG	CAGATGTTTG	GCTATACCAA	GCTGCCCGAA	GAGCCTAAAG
251	GCATCCGCGT	GATTTACGTT	ACCGATATGG	GCAATGTTAC	CGATTGGACG
301	AATCCCAATG	CCGACACGGA	GTGGATGGAT	GCGAAAAAAG	CCTTTTACGT
351	CATCGACAGC	GGCTTTATCG	GCGGTATGGG	TGCGGAAGAC	GCGCTGCCGT
401	TCGGCAACAA	AGAGCAGGCT	GAGAAATTG	CAAAGGATAA	AGGCGGTAAG

```

1  MKKTLAIVA VSALSXCRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDGGK
151 VVGFDMPDPT YIFK*

```

ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m915.pep	MKKTLLAIVAVSALSACRQAE	EGPPPLPRQISDRSVGHYCS	MNLTEHNGPKAQIFLNGKP			
g915	MKKTLLAIVAVFALSACRQAE	EAPPPLPRQISDRSVGHYCS	MNLTEHNGPKAQIFLNGKP			
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMF	GYTKLPEEPKGI	RVIYVTDMGNV	TDWTPNADTEW	MDAKKAFYVIDS	
g915	DQPVWFSTVKQMF	GYTKLPEEPKGI	RVIYVTDMGNV	TDWTPNADTEW	IDAKKAFYVIDS	
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALP	FGNKEQAEKFAK	DKGGKVVGFD	DMPTDYIFKX		
g915	GFIGGMGAEDALP	FGNKEQAEKFAK	DKGGKVVGFD	MPDAYIFKX		
	130	140	150	160		

1	ATGAAAAAAA	CCCTGTTGGC	AATTGTTGCC	GTTTCGCCT	TAAGTGCGCTG
51	CCGGCAGGCG	GAAGAGGGAC	CGCGCCTTT	ACCCCGGCAG	ATTAGCGACC
101	GTTCGGTCCG	ACACTATTGC	AGTATGAAC	TGACCGAACA	CAACGGCCCC
151	AAAGCCGACA	TTTTCTTGAA	CGGCAAAACC	GATCAGCCCG	TTTGCTTCTC
201	CACCATCAAG	CAGATGTTCC	GCTATACCAA	GCTGCCCGAA	GAGCCTAAG
251	GCATCCGCGT	GATTTACGTT	ACCGATATGG	GCAATGTTAC	CGATTGGACG
301	AATCCCAATG	CCGACACGGA	GTGGATGGAT	GCGAAAAAAG	CCTTTTACGT
351	CATCGACAGC	GGCTTTATCG	CGGGTATGGG	TGCGGAAGAC	GCGCTGCCGT
401	TCGGCAACAA	AGAGCAGGCT	GAGAAATTTG	CATAGGATAA	AGGCGGTAA
451	GTTGTCGGTT	TCGACGATAT	CGCTGATACC	TATATTTTCA	AATAA

```

1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDGGGK
151 VVGFDMPDT YIEF*

```

	10	20	30	40	50	60
m915.pep	MKKTLLAIVAVSALSXCRAE	EGPPPLPRQISDRSVGHYCS	MNLTEHNGPKAQIFLNGKP			
a915	MKKTLLAIVAVSALSACRAE	EGPPPLPRQISDRSVGHYCS	MNLTEHNGPKAQIFLNGKP			
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMF	GYTKLPEEPKGI	RVIVTDMGNVD	DWTNPNADTEW	MDAKKAFYVIDS	
a915	DQPVWFSTIKQMF	GYTKLPEEPKGI	RVIVTDMGNVD	DWTNPNADTEW	MDAKKAFYVIDS	

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccact cgcCGTCctg actgctTtgc tgcttgccagc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaaa
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCCG
251 GTTACGACAT TGTGCGCCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCCTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTTG ATGGAGGACG
1001 AATTTAAGAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCTAT CCGGCCGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKQNG IKVTYDVYDS DETLESKVL T GSKGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKALGTD KLPDQNDLV FNPEYTFKLK QCGISYLD SA AEIYPMVLNY
201 LKGNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCTVTIGF
251 GGDLNIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCC T GGCCGTCTG ACTGCTTGC TGCTTGCCAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTGCGCCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTTGGTG TTGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

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1314

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751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAATAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCTCTGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAAGTGCAG GATGTGAAGG CGGGGAAATA A
```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

```
1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51 TVADFEKKNG IKVTYDVYDS DETLESKVLTKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLDLS AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLNIAKRR AEEAGGKEKI RVMPKKEGVI IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAENQNVLKIYNWSEYVDPETVADFEKKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAENQNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLDLSAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLDLSAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRRAEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRRAEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNFSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARDLMEDEFKNDNTIFPSGEDLKNFSFIMVPIRPA					
	310	320	330	340	350	360

370

1315

m917.pep ALKFMVRQWQDVKAGKX
 |||||
g917 ALKFMVRQWQDVKAGKX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
1 ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACAGC
51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
101 ACCGAAACGT ATTGAAATTT TACAACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAATA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCTG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCCGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GCGCGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
51 TVADFEKKNQ IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLDIA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNEFTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVFIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAEQNVLKIYNWSEYVDPETVADFEKKNQ					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAEQNVLKIYNWSEYVDPETVADFEKKNQ					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
a917	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
	130	140	150	160	170	180
m917.pep	QCGISYLDIAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA					
a917	QCGISYLDIAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	QCGISYLDIAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA					
a917	QCGISYLDIAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA					

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a917      QCGISYLDAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVI PKDAKNVANAHK
           |||||||
a917      RGDTTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVI PKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVITYAPSSKPA RELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           |||||||
a917      YINDFLDPEVSAKNGNFVITYAPSSKPA RELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           |||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGGCAAAAGC CTGCAATCCT
251 TCCGCTCCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGCCCCAAG CCTTTCAAAC CCCCGTGCA TCCCTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAAC GGGCCCGCTT CCCGATTIAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCGCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaggCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCGgcgTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTTCATGCAC AtccaaggCT CGGGCCGCT
801 GAAAAACCcg tccggcaaat acatCCGCat cggTaagcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGTCCG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKCHLLRSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTEARFPFIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIRGR FEGRFLPYH TRNQINGGAL DGRAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGFPVGAIG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:

1	MKKYLFRAAL	YGIAAAAILAA	CQSKSIQTFF	QPDTSVINGP	DRPVGIPDPA
51	GTTVGGGGAV	YTVVPHLSLP	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAQAFQTPVH	SFQAKQFIFV	YFTPVQVAGN	GSLAGTVTGY	YSPVLKGGDR
151	RTAQARFFPI	GIPDDFISVP	LPAGLRSGKA	LVRIRQTGKN	SGTIDNTGGT
201	HTADLSRFPI	TARTTAIKGR	FEGSRFLPHY	TRNQINGAGL	DGKAPILGYA
251	EDFVELPFMH	IQSGSRLKTP	SGKYIRIGYA	DKNEHPYVSI	GRYMADKGYL
301	KLKGTSYQGI	KSYMQRNPQR	LAELVGQNSP	YIFFRELASG	SNDGPFVAGL
351	TPLMGEYBQA	VDRHYITLGA	PLFVATAHPV	TRKANLRLIM	AQDTGSAIKG
401	AVRVDYFWGY	GDEAGELAGK	OKTTGYVWOL	LPNGMKPYER	P*

	10	20	30	40	50	60
m919.pep	MKKYLFR	AALYGLIAAA	ILAACQSKSI	QTFFPQPD	TSVINGPDR	FPVGIPDPAGTTVGGGGAV
	:	:	:	:	:	:
g919	MKKHLLRS	ALYGLIAAA	ILAACQSR	SIQTFFPQPD	TSVINGPDR	PAGIPDPAGTTVAGGGAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLS	PLPHWAAQD	FAKSLQSF	RLGCANL	KNRQGWQD	VCQAQAFQTPVHSFQAKOFFER
	:	:	:	:	:	:
g919	YTVVPHLS	PLPHWAAQD	FAKSLQSF	RLGCANL	KNRQGWQD	VCQAQAFQTPVHSFQAKRFFER
	70	80	90	100	110	120

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	130	140	150	160	170	180
m919.pap	YFTPWQVAGNGSLAGTVTGYEFPVLKGD	DRRTAQARFPIYGIPDDFISVPLPAGLRSGKA				
g919	YFTPWQVAGNGSLAGTVTGYEFPVLKGD	GRRTERARFPIYGIPDDFISVPLPAGLRGGKN				
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pap	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pap	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI	GRYMADKGYL				
g919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI	GRYMADKGYL				
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pap	KLGGTSMQGIKSYMQRNPQRLAEVLGQNP	SYIFFREL	AGSSNDGPV	GALGTPLMGEYAGA		
g919	KLGGTSMQGIKSYMQRNPQRLAEVLGQNP	SYIFFREL	AGSSNDGPV	GALGTPLMGEYAGA		
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pap	VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pap	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT ACCTATTC CGCGGCCCTG TCGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCGCC
151 GGAACGACGG TCGCGCGCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT CGCCAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGGCCAAG CCTTTC AAC CCGTCCAT TCCGTTCAGG CAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TCGAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCATC ACTGCGGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCTT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGCGCGCTT GACGGCAAAG CCCCATACT CGGTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTGG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG

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1319

```
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```
1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPR LAEVLGQNPS YIFFRELTGS SNDGFPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep MKKYLFRALYGI AAILAACQSKSIQTFPQDTSVINGPDRPVGIPDPAGTTVGGGGAV
|||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQDTSVINGPDRPVGIPDPAGTTVGGGGAV
      10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFOAKQFFER
|||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
      70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
|||||
a919      YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
      130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
|||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
|||||
a919      DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
      250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGFPVGALGTPLMGEYAGA
|||||
a919      KLGQTSMQGIKAYMQQNPRLAEVLGQNPSYIFFRELTGSSNDGFPVGALGTPLMGEYAGA
      310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
|||||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      370     380     390     400     410     420

      430     440
m919.pep QKTTGYVWQLLPNGMKPEYRPX
|||||
a919      QKTTGYVWQLLPNGMKPEYRPX
      430     440
```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTCCGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCT GGAAATCGTC
301 CCGCTGGACA ATCccgccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtaccAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT cGacaccac cgacggcgaa ggCGaagtgg acatcatCCC
501 CTTGCgccaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAttctcc
551 CCGATcaaAG CCTGTGccga AAACAggcgA ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAEY QTPFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCGCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTAAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFFDQSVK
 251 QKQANYSTLT FQIGHSHH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920.pep				PMQLVTEKGKENMIQ	RGTYNYQYRSNR	FPVK
m920	GGEYLKADLGYGEFPELEPIAKDRLHIFSKPMQLVTEKGKENMIQ	RGTYNYQYRSNR	FPVK			
	40	50	60	70	80	90
g920.pep	DGSYLVTAEYQPTFRSKNKAGWKQAGIKEMP	DASYCEQTRMFGKNIVNVGHESADTAII	IT			
m920	DGSYLVTAEYQPTFRSKNKAGWKQAGIKEMP	DASYCEQTRMFGKNIVNVGHESADTAII	IT			
	100	110	120	130	140	150
g920.pep	KPVGQNLEIVPLDNPADIVHVGKRFKVRVLF	RGEPNATVTATFDGFDTS	DRSKTHKTEA			
m920	KPVGQNLEIVPLDNPANIVHVGKRFKVRVLF	RGEPNATVTATFDGFDTS	DRSKTHXXEA			
	160	170	180	190	200	210
g920.pep	QAFSDTTDGEGEVDIIPLRQGFWKASVEYKAD	FPDQSLCRKQANYTT	TLTFQIAHSHHX			
m920	QAFSDSTDDKGEVDIIXLRQGFWKANVEHK	TDFPDQSVCKQANYSTLT	FQIGHSHSHX			
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920.seq

1	TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCGCATC
51	CGCCACGCC	CACCGCGTCT	GGGTGGAAC	CGCCACACG	CACGGCGGCG
101	AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTCCCGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGGC	AAGGAAAACA	TGATTCAACG	CGGCACATAC	AACTACCACT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTCTGGTC	AAAAAACAAA	GCAGGCTGGA	AACAGGCGGG
351	CATCAAAACA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTCC
401	GCAAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
451	ACCAAACCGG	TCGGACAAAA	CTTGGAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTCAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTTCTG	TTCCGTGGCG
551	AACCGCTGCC	CAATGCCACC	GTTACCGCCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTGCGC	CAAGGCTTCT
701	GGAAGCCCAA	TGTCGAACAC	AAAGCCGACT	TCCCGGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTTCGA
801	CCATTAA				

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920.pep

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDRHLHIF	KPMQLVTEKG	KENMIQRTY	NYQYRSNRPV	KDGSYLVAIE
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	RMFGKNIVNV	GHESADTAII
151	TKPVGQNLEI	VPLDNPANIH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFDT
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIPLR	QGFWKANVEH	KADFFDQSVK
251	QKQANYSTLT	FQIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
a920	XKKTLLTLLAVSALFAASAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMIQRGTINYQYRSNRPVKDGSYLVIAEYQPTFWSKXKAGWKQAGIKE					
a920	KPMQLVTEKGKENMIQRGTINYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
a920	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTATFDGFDTSDRSKTHXXEAQAFSDSTDDKGEVDIIXLRQGFWKANVEH					
a920	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQSVQCQKQANYSTLTFQIGHSHHX					
a920	KADFPDQSVQCQKQANYSTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA  CATTGACACT  GCTCGCcggt  TcCGCACTAT  TTGCCACATc
51  cgCaCACCCC  CACCgCGTCT  GGGTCGAAAC  CgcccCACAg  cAcgGCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTCCCCGA  ACTCGAACCC
151 ATCGccAAAG  ACCgcccTGA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGT  AAGGAAAACA  TGATTCAACG  CGGCACATAC  AACTACCAAT
251 ACCGCAGCAA  CCGTCCCCTC  AAAGACGGCA  GCTACCTCGT  TACCGCCGAA
301 TATCAGCCTA  CTTTCCGGTC  AAAAAACAAA  GCAGGCTGGA  AACAGGCTGG
351 CATCAAAGAA  ATGCCTGACG  CAAGCTATTG  CGAACAAACC  CGTATGTTTC
401 GTAAAAACAT  TGTC AACGTG  GGACACGAAA  GCGCGGACAC  CGCCATCATC
451 ACCAAACCGG  TCGGACAAAA  CTTGGAAATC  GTCCCGCTGG  ACAATCCCGC
501 CAACATTCAC  GTAGGCGAAC  GCTTCAAAGT  CCGCGTTCTG  TTCCGTGGCG
551 AACCGCTGCC  CAATGCCACC  GTTACCGCTA  CATTTGACGG  CTTTCGACAC
601 AGCGACCGCA  GCAAAACGCA  CAAAACCGAA  GCCCAAGCCT  TCTCCGACAC
651 CACCGACGGC  AAAGGCGAAG  TGGACATCAT  CCCCTTGCGC  CAAGGCTTTT
701 GGAAGCGGAG  TGTCGAATAC  AAAGCCGATT  TCCCGGATCA  AAGCCTGTGC
751 CAAAAACAGG  CGAACTACAC  AACTTTAACC  TTCCAATCG  GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV  SALFATSAP  HRVWVETAHT  HGGEYLKADL  GYGEFPELEP
51  IAKDRLHIFS  KPMQLVTEKG  KENMIQRGTY  NYQYRSNRPV  KDGSYLVTAE
101 YQPTFRSKNK  AGWKQAGIKE  MPDASYCEQT  RMFGKNIVNV  GHESADTAII
151 TKPVGQNLEI  VPLDNPANIH  VGERFKVRVL  FRGEPLPNAT  VTATFDGFDT
201 SDRSKTHKTE  AQAFSDTTDG  KGEVDIIPLR  QGFWKASVEY  KADFPDQSLC
251 QKQANYTTLT  FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA  CATTGACACT  GCTCGCCGTT  TCCGCCCTAT  TTGCCACATC
51  CGCCACGCCC  CACCGCGTCT  GGGTCGAAAC  CGCCACACG  CACGGCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTCCCCGA  ACTCGAACCC
151 ATCGCCAAAG  ACCGCCTGCA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGC  AAGGAAAACA  TGATTCAACG  CGGCACATAC  AACTACCACT
251 ACCGAAGCAA  CCGTCCCCTT  AAGGACGGCA  GTTACCTCGT  CATCGCCGAA

```

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```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAACCGGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTGGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GTCATTGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

```

m920-1.pep
1  MKKTLTLLAV SALFATSAAH HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRHLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAQFSDSTD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/g920-1 96.3% identity in 268 aa overlap

          10      20      30      40      50      60
m920-1.pep MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRHLHIFS
          |||
g920-1      MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRHLHIFS
          10      20      30      40      50      60

          70      80      90      100     110     120
m920-1.pep KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
          |||
g920-1      KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE
          70      80      90      100     110     120

          130     140     150     160     170     180
m920-1.pep MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
          |||
g920-1      MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
          130     140     150     160     170     180

          190     200     210     220     230     240
m920-1.pep FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAQFSDSTD KGEVDIIPLRQGFWKANVEH
          |||
g920-1      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAQFSDTD KGEVDIIPLRQGFWKASVEY
          190     200     210     220     230     240

          250     260     269
m920-1.pep KTDFFDQSVCKQKQANYSTLT FQIGHSHHX
          |||
g920-1      KADFFDQSLCQKQANYTTLT FQIGHSHHX
          250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

```

a920.seq
1  TGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51  CGCCCACGCC CACCGCTGCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAACCGGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTGGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GCCATTGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```

a920.pep
1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRTY NYQYRSNRPV KDGSYLVIIE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TRPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/a920 98.9% identity in 267 aa overlap

m920-1.pep      10      20      30      40      50      60
m920-1.pep      MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
a920             XKKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
m920-1.pep      10      20      30      40      50      60
a920             10      20      30      40      50      60

m920-1.pep      70      80      90      100     110     120
m920-1.pep      KPMQLVTEKGKENMIQRTYNYQYRSNRPVKDGSYLVIIEYQPTFWSKNKAGWKQAGIKE
a920             KPMQLVTEKGKENMIQRTYNYQYRSNRPVKDGSYLVIIEYQPTFWSKNKAGWKQAGIKQ
m920-1.pep      70      80      90      100     110     120
a920             70      80      90      100     110     120

m920-1.pep      130     140     150     160     170     180
m920-1.pep      MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLIVPLDNPANIHVGERFKVRVL
a920             MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLIVPLDNPANIHVGERFKVRVL
m920-1.pep      130     140     150     160     170     180
a920             130     140     150     160     170     180

m920-1.pep      190     200     210     220     230     240
m920-1.pep      FRGEPLPNATVTATFDGFDSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
a920             FRGEPLPNATVTATFDGFDSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
m920-1.pep      190     200     210     220     230     240
a920             190     200     210     220     230     240

m920-1.pep      250     260     269
m920-1.pep      KTDFFDQSVQCQKQANYSTLTFQIGHSHHX
a920             KADFPDQSVQCQKQANYSTLTFQIGHSHHX
m920-1.pep      250     260
a920             250     260

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```

g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51 Ccagtctatt tatGtgccca cattgacgga aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGCTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggaA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```

g921.pep
1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51 HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMKMQP LK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```

m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA

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251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
 101 YEIYLRSID SQRGAITEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSIDSQRGAITEQ					
	:					
g921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSIDVDSQRGEITEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	:					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAT ACCTTATCCC TCTTCCATT GTGGCAGTTC TTTCCGGCTG
 51 CCAGTCTATT TATGTGCCA CATTGACGGA AATCCCCGTG AATCCTATCA
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTCCGCCT TGCCTCTTCG
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
 101 YEIYLRSID SQRGAITEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m921 . pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921 . pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922 . seq

```

1   ATGGAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTGTG GACGATGAAG TCGGGAAGG GGATTTTTC CAGCGCGAAT
251 GGCAGGATTT TTTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATt
301 ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAAa
351 ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaAacc
401 gcgcggttat cgatgatgtg gcgCAAAAat acggcgtGCC TGCCGAGCTT
451 ATCGTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGGTT TTTCCAAAAA GAATTGGTCG AGCTTTTAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTTATGC CTTGAGCTA CCGGAAATGG GCGGTGATT
701 ATGAcgggga cggacatCGG GATATatggg GCAACGTcgg tgatgtecg
751 gcatcggTTG CCAATTatga gaagCAGCAC GGTGGCGCA CgggcggTAA
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CaggcAATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGACGG TGGCGGATTT GAaggCGTAc
901 ggcacatccc ccggggaaac GCTCGCAGAT GATGAAAAGg cgGTTTGTGTT
951 CAACTGGAA ACCGCACCCG GCGTGTGTTGA ATATTATTG GGCTTGAACA
1001 ATTTTATAC GGTATGGCAG TACAACCACA GCCGATGTA TGTAAcgcg
1051 gtcaggGACA TTGCCAATTC GCTCGCGCGC CCGGATGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922 . pep

```

1   MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVGKGFDF QAEWQDFFDK AAYKADIVKI
101 MHRPSTSRPW YVFRGTNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151 IVAIIGIETN YGKNTGSFRV ADALATLGFD YPRRAGFFQK ELVELLKLAK
201 EEGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANVMQKH GWRTGGKMLV SATLAPADV QAIIGEKTAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMYVTA
351 VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922 . seq

```

1   ATGAAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACGCCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATTT CCGGCAAGGC GAAATTTCCG GCGCGCGGCC
401 GGTTTATATG GGAACCCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCTCG CCGAATTAT CGTGGCGGTT ATCGGATTG AAACGAATTA
501 CCGCAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG GCCGGGTTTT TCCAAAAAGA ATTGGTCGAG

```

m922.ppt

m922/g922

```

10      20      30      40      50      60
m922.pep MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAFDAAAVFDAAAVP
          :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g922      MEKRKILPLAICLAALSACTAMEARTPRANEQAQAPRADEMKKESRPAFDAA-----AVP
          10      20      30      40      50

70      80      90      100     110     120
m922.pep VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAKADIVKIMHRPSTSRPWYVFR
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g922      VSDSGFAANANVRRFVDDEVGKGDFSQAEWQDFFDKAAKADIVKIMHRPSTSRPWYVFR
          60      70      80      90      100     110

130     140     150     160     170     180
m922.pep TGN SGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g922      TGN SGRAKFHGARRFYAENRAVIDDVAQKYGVPAELIVAIIGIETNYGKNTGSFRVADAL
          120     130     140     150     160     170

190     200     210     220     230     240
m922.pep ATLGF DYPRRAGFFQKELVELLKLAK EGGDVFAFKGSYAGAMGMPQFM PSSYRKWAVDY
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g922      ATLGF DYPRRAGFFQKELVELLKLAK EGGDVFAFKGSYAGAMGMPQFM PSSYRKWAVDY
          180     190     200     210     220     230

250     260     270     280     290     300
m922.pep DGDGHRDIWGNVG DVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAI IGEKTALTRTV
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g922      DGDGHRDIWGNVG DVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAI IGEKTALTRTV
          240     250     260     270     280     290

310     320     330     340     350     360
m922.pep ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTVAVRDI
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g922      ADLKAYGIIPGETLADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTVAVRDI

```

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	300	310	320	330	340	350
m922 . pep	370					
	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1  ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACGCCGCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATT CCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAAAACCGC GCGTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CCGCAAAAT ACGGGCAGT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG GCCGGGTTT TCCAAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTCG CCTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TACTGGTGTC TGCAACATTG GCGCGGGTG
851 CGGATGTTCA GGCAATCAT GCGGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGA AGCGGTACG CATCATCCC GCGGAAGAGC TTGCCGATGA
951 TGAAAGGCG GTTTGTTC AACTGGAAAC CGCACC CGC GTGTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACG TATGGCAGTA CAATCACAGT
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTTCG TTGGCGGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KKE SRPAFDA
51  AAVFDAAAVP VDSGFAANA NVRRFVDEV GKGDFSRAEW QDFFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPAELIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKEEGG DVFAFKG SYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHWRT GSKILVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYLLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922 . pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKE SRPAFDAAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMKKE SRPAFDAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922 . pep	VDSGFAANANVRRFVDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
a922	VDSGFAANANVRRFVDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922 . pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKALTRTV
          ||||||||||||||||:||||||||||||||:||||||||||||||
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRTGGKILVSATLAPGADVQAIIGEKALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          ||||||||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCCG
201 CGGTTGGACG GCGGCATACT TGGGTAGTAG GATGTTCAGG CATAAAACGG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGA CTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTC GTTCCGCCCG AACTTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAVR
51  GKRRIP EHL LLLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRLTVSGNV
101 LATCILIDYF VPPEL FVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGTATT TCGGCAGCAT GACATTCAA CATAAGACAG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGA CTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTGTGAC TGTCTGCGGC TTCGTCGCCT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATTT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCAR
51  GQRRIP EHL LLLPALGGWV GAYFGSMTFK HKTAKKRFV LFRLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

```

      10      20      30      40      50      60
g923.pep  MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRVRGKRRIP EHR L
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m923      MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRC A I R G Q R R I P E H R L
          10      20      30      40      50      60

      70      80      90      100
g923.pep  LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFR LTVSGNVLATC I L I D -----
          ||||| : ||| : ||| : ||| : ||||| ||||| ||||| ||||| |||||
m923      LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFR LTVSGNVLATL I L I Y S G L N L N Q Y G V A S
          70      80      90      100      110      120

                                110      120
g923.pep  -----YFVPPELFVKLGQHLX
          ||||| : ||||| :
m923      PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX
          130      140      150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

```

1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTCTGTC
51 TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAACGCGG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCTG CTGCTGCCTG CCTTGTTGCG
201 CCGTTGGGCG GCGGCATACT TGGGCAGCAG GATATTCAGG CATAAACCGG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGA CTGTTT C GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTGTA CTGTCTGCGG CTTCGTGCGC
451 TTGTCTGAT TTTTGTAAAT CCACTAT.AT TATTTTGTCC CGCCTGAATT
501 TTTCTGAAAA CTCGGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

```

1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLEYAFAL YGIDKRRAVR
51 GKRRIP E H R L L P A L F G G W A G A Y L G S R I F R H K T A K K R F V V L F R L T V S G N V
101 L A T L I L I Y S G L N L N Q Y G V A S P X A Q R E R F S K V L K H Q V N R F R T I C T V C G F V A
151 L S * F L L I H Y X Y F V P P E F F V K L G Q N T *

```

m923/a923 84.6% identity in 175 aa overlap

```

      10      20      30      40      50      60
m923.pep  MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRC A I R G Q R R I P E H R L
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a923      MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRAVRGKRRIP E H R L
          10      20      30      40      50      60

      70      80      90      100      110      120
m923.pep  LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFR LTVSGNVLATL I L I Y S G L N L N Q Y G V A S
          ||||| : ||| : ||| : ||| : ||||| ||||| ||||| ||||| |||||
a923      LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFR LTVSGNVLATL I L I Y S G L N L N Q Y G V A S
          70      80      90      100      110      120

                                130      140      150      159
m923.pep  PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a923      PXAQRERFSKVLKHQVNRFTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX
          130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

```
g925.seq
  1 ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcGCGGTGT TGGCGGGCTG
 51 CGGCAaggat gcCGGCGGtt acgagggTtA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTttACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGGCG
351 ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

```
g925.pep
  1 MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
 51 KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKGQTA QAYLDARNAL PSNQTYYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

```
m925.seq (partial)
  1 ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
 51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAGAGGG TATGATTGCC GTCAAAAAG AAAAAGGCAA TTACTTCCTT
.....
```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

```
m925.pep (partial)
  1 MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
	:				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKGQT				
	60	70	80	90	100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

```
g925-1.seq
  1 ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
 51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTttACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGGCG
351 ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51 KINVFTGKEE SLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAG
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51 NKIHVVTGKE ESLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKE					
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQT					
g925-1	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX					
g925-1	AQAYLDARNALPSNQTYQQRQAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51 AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAG
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTCAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAAAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1		AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKEESMLLSEKDGALSINTGIGE		
	30	40	50	60
	70	80		
	40	50	60	70
	80	90		

1333

```

a925-1.pep  IPIKLSDDGKELYVERROYVKTDAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
|||||
m925-1      IPIKLSDDGKELYVERROYVKTDAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
          90      100      110      120      130      140

          100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
          150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTGC AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGGCGCGC CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGaa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAE
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGWTIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTGC AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGAAAGT
301 GCGGAAGAAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGGCGCGC CCTTACC GCA
401 TCTGCCCCGA CGGCATATTG GAACAATACG GTTGACTGT GTGCGAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCAGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAE
101 ABELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGWTVGRT
151 ADSSGQVRTL QLNNGNLNR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

          10      20      30      40      50      60
g926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
|||||
m926      MKHTVSASVILLTACAQLPQNNENLWQPSSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEATEDLSRQLVGFKLPIQYLHI
|||||
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAELSRQLVGFKLPIQYLHI
          70      80      90      100     110     120

          130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGWTIGQNCRWGASPNVATE

```

1334

m926
 ||:|||||:|||||:|:|:|
 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
 130 140 150 160 170 180

a926.seq
 1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
 51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
 101 GCAGTTTCAC GCGGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
 151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
 201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
 251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGGAAGT
 301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
 351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CCTTACCACA
 401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGACTGT CGGCAGAACC
 451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
 501 GAACATCAGG CTGGTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
 551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep
 1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEKGK
 51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
 101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
 151 ADSGGQVRTL QLNNGNLNR LVFTEIGMPS ETETQECAA RIQ*

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASV	LLLLTACAQLP	QNNENLWQPS	EHIS	FFAAEGR	LAVKAEKGKSYANFDWTYQ
a926	MKHTVSASV	LLLLTACAQLP	QNNENLWQPS	EHTRSFTAEG	RLAVKAEKGK	SYANFDWTYQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININT	PLGSTLGQLC	QDRDGALAVD	GKGNVYQAES	AEELSRQLVG	FKLPIQYLHI
a926	PPVETININT	PLGSTLGQLC	QDRDGALAVD	GKGNVYQAES	AEELSRQLVG	FKLPIQYLHI
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
a926	ETETQECAAARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq
 1 atgaaaacct acGCACaggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
 51 CAGCCCcgca GCcgatTcaa accaTCCGTC CGGAcAaaAT GCCCCGGCCA
 101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTcgtacgat
 151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaaCATA
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
 251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

g927.ppt

1	MKTYAQALYT	AALLTACSPA	ADSNHPSGQN	APANTESDGK	NITLLNASYD
51	VTRYFYKEYD	HLFVGTYQSE	HPGTSVSIQQ	SHGGFSKQAL	SVANGLQADV
101	DTWQSSQSID	LLEKXGLVEK	GWQQALPDHA	APYTSTMVFL	VRKNNPKQIR
151	VDNMLAKDGV	NIVIAKTSGN	GRYAFGLGAY	YGLKANNGNE	QEAQKLVASI
201	LKNTLPVFENG	GRXPPPPPSH	NATSATYSYL	LKTKPTTSAK	N*

m927.seq

1	ATGAAAACCT	ACGCACCGGC	ACTCTATACC	GCAGCCCTGC	TCACCGCCTG
51	CAGCCCGCA	GCCGATTCAA	ACCATCCGTC	CGGACAAAAT	GCCCCGGCCA
101	ATACCGAATC	CGACGGAAAA	AACATTACCC	TGCTCAACGC	CTCATACGAT
151	GTGGCAGCG	ATTTTTCAC	AGAATAACA	CCCTTATTTA	TCAAAACATA
201	CCAATCCGAA	CACCCCGCCA	CATCCGTCAG	ATCCACAAG	TCCCACGGCG
251	GCTCCAGCAA	ACAGGCATTA	TCCGTAGCCA	ACGGCCTTCA	AGCCGATGTC
301	GTAACCATGA	ACCAATCCTC	CGACATCGAC	CTGCTCGAAA	AAAAAGGACT
351	GGTAGAAAAA	GGCTGGCAAC	AAGCCCTCCC	CGACCACGCC	GCGCCCTACA
401	CCAGCACTAT	GGTTTCTCTT	GTCCGAAAA	ACAACCCCAA	ACAGATCCCG
451	GATTGGAACG	ACCTTGCCAA	AGACGGCGTT	AACATCGTCA	TGCCCAATCC
501	CAAAACCTCG	GGCAACGGAC	GCTACGCTTT	CCTCGGCGCA	TACGGTTACG
551	GTCTGAAAAC	CACCAACGGC	AACGAACAGG	AAGCCCAAAA	ACTCGTCGCA
601	TCCATCCTCA	AAAACACCC	CGTTTTTGAA	AACGGCGGAC	GckCgCCACC
651	ACCACCTTCA	CACAACCGCA	CATTCGGCGAC	GTACTCATCA	CTTTTGAAAA
701	CGAAGCCAAC	TACGTGACGr	AAAAACTGA		

m927.ppt

1	MKTYAPALYT	AALLTACSPA	ADSNHPSGQN	APANTESDGK	NITLLNASYD
51	VARDFYKEYN	PLFTKTYQSE	HPGTSVSIQQ	SHGGSSKQAL	SVANGLQADV
101	VTMNQSSDD	LLEKKGVLVEK	GWQOALPDHA	APYTSTMVFL	NRQNNPKQIR
151	DWNLDAKDG	NIVIANPKTS	GNRGYAFGLA	YGYGLKTTNG	NEQEAQKLVA
201	SILKNTVPVE	NGGRXPPPPS	HNATSATYS	LLTKTPPTSA	KN*

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

q927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQA	LYTAALLTACSPAADSNHPSGQNAPANTESD	GKNITLLNASYDVTRYFYKEYD			
m927	MKTYAPALY	TAALLTACSPAADSNHPSGQNAPANTESD	GKNITLLNASYDVARDFYKEYN			
	10	20	30	40	50	60
	70	80	90	100	110	120
g927.pep	HLFVGTYQSEHPGTSVSIQQSHGGFSKQALS	VANGLOADVVTM	NQSSDIDLLEKXGLVEK			
	:					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALS	VANGLOADVVTM	NQSSDIDLLEKKGGLVEK			
	70	80	90	100	110	120
	130	140	150	160	170	
g927.pep	GWQQALPDHAAPYTSTMVFLVRKKNPKQIRD	WNDLAKDGVNIVIA--KTS	GNNGRYAFLGA			
m927	GWQQALPDHAAPYTSTMVFLVRKKNPKQIRD	WNDLAKDGVNIVIANPKT	SGNGRYAFLGA			
	130	140	150	160	170	180

1336

```

      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTS
          |||||:|||||||||||||||||||||||||||||||||||||||||
m927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          |||
m927      AKNX
          240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAACCT ACGCACC GGC ACTCTATACC GCAGCCCTGC TCAGCGCCTG
51  CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCACGGG ATTTTACAA AGAATAACAAC CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAAA ACAACCCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCAATCC
501 CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
601 TCCATCCTCA AAAACACCCC CGTTTTGAA AACGGCGGAC GCGCGCCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGAAAA
701 CGAAGCCAAC TACGTCAGCA AAAAATG

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT AALLSACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51  VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
201 SILKNTPVFE NGGRAPPPPS HNATSATYSS LLKTKPTTSA KN*

```

m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:|||||||||||||||||||||||||||||||||||||||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          |||||:|||||||||||||||||||||||||||||||||||||||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:|||||||||||||||||||||||||||||||||||||||||
a927      GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTSA
          |||||:|||||||||||||||||||||||||||||||||||||||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

```

m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq

```

1  ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACgctggg CATCGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GCGGCACTTA TACATCcgAT TATGCagtcg attgCcgCA GttacggctC
501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
551 tcaattaTCA TTCcaatCCC atttcgctgg ctAtggctat taCTGcaact
601 gCCCCcaaCC CTTAATcgt caacttgatt gccGaaaaTt taggcagtag
651 tttccgtCTT Tcttgggggg cgTGGGcgtg ggcaaTGGCT Gttcccgcg
701 ttatcgccctt TtctgTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGCTGAG
801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGAATTGGGA CGATGTTTTG AAAGAAAAAA
1001 CGCGGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT TAGGGCCGA
1051 TTTTtaAATA AActcggact gattaaatGG TTCTCCGAG TGTGGCGGA
1101 AagtgtcggC GGTtTGGGCG TTAGCGGCAC GGCTGCGGCG GTAATCCTCG
1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTCTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
1301 TGACCCCTAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTGGG TGGAAAGTTC
1451 TGGGATATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep

```

1  MKLGFKPIPL AIAAVLCLV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
151 GGIHPIMQS IAGSYGSNPA KTEGKMGKY LALVNYHNP ISSAMAITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLA MYA HYMFASSTAH
401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq

```

1  ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCGGTT TTTGGAAGAA AAACGCTGGG CATCGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

```


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```

451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCGCTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATT TATATTTwyT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGA CTGTTGGA CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTCCGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGCG GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTTTCGCT GCTGCCGTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTTCG
1351 GCCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTTC TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLA MYA HYMASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

```

          10      20      30      40      50      60
g929.pep  MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKVMPLGALSII
          |||||
m929      MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKAMPLGALSII
          10      20      30      40      50      60

          70      80      90      100     110     120
g929.pep  AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIYLFIAV
          |||||
m929      AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIYLFIAV
          70      80      90      100     110     120

          130     140     150     160     170     180
g929.pep  FGRKTLGIGYSLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY
          |||||
m929      FGRKTLGIGYSLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY
          130     140     150     160     170     180

          190     200     210     220     230     240
g929.pep  LALVNYHNSPISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM
          |||||
m929      LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM

```

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	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGVGSGTAAGVILVLAIFYAHYMFASSTTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGVGSGTAAGVILVLAIFYAHYMFASSTTAHITAMFGAFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

a929.seq

```

1  ATGAAATTGG  GTTTCAAACC  GATACCCCTC  GCCATTGCCG  CAGTATTGTG
51  CGCCTTGTT  TTGGCACTGC  CCGTACCCGA  CGGGGTCAAG  CCTCAGGCTT
101  GGACGCTGCT  GGCCATGTTT  ATCGGTGTGA  TTGCCGCCAT  TATCGGCAAG
151  GCCATGCCGT  TGGGTGCGCT  GTCGATTATT  GCCGTGCGGT  TGGTCGCAGT
201  AACCGGCGTA  ACCGCCGACA  AACCGGGTGC  GCGCATGAGC  GATGCGTTGA
251  GTGCGTTCGC  CAATCCGTTG  ATTTGGCTGA  TTGCCATCGC  AGTTATGATT
301  TCGCGCGGTT  TGCTCAAAAC  AGGGCTGGGG  ATGCGTATCG  GATATTGTGT
351  TATCGCCGTT  TTTGGAAGAA  AAACGCTGGG  CATCGGTTAC  AGTCTCGCTC
401  TTTCCGAAC  TCTGCTGGCT  CCCGTTACCC  CTTCCAATAC  CGCGCGCGGC
451  GCGCGCATTA  TACATCCGAT  TATGCAGTCG  ATTGCCGGCA  GTTACGGCTC
501  CAATCCCGCA  AAAGGCACAG  AAGGCAAGAT  GGGTAAATAT  TTGGCTTTGG
551  TCAACTATCA  TTCCAATCCC  ATTCGTCGG  CTATGTTTAT  TACTGCAACT
601  GCGCCCAACC  CTTTAATCGT  CAACTTGATT  GCCGAAAATT  TAGGCAGTAG
651  TTTCCGTCTT  TCTTGGGGGG  CGTGGGCGTG  GGCAATGGCT  GTTCCCGCGC
701  TTATCGCCTT  TTTCTGTATG  CCTTTGATTT  TATATTTTTT  GTATCCGCCT
751  GAAATTAAAG  AAACGCCCAA  TGCCGTTCAA  TTTGCCAAAG  ACCGCTGAG
801  GGAGATGGGT  AAAATGTCGG  CAGACGAAAT  CATTATGGCG  GTCATTTTCG
851  GTATCTTGTT  GCTGTTGTGG  GCAGATGTTT  CCGCCCTTAT  TACCGGCAAT
901  CACGCTTTTA  GTATCAACGC  CACCGCCACC  GCATTTATCG  GATTAAGCCT
951  GCTTTTGCTT  TCCGGTGTAT  TGACTTGGGA  CGATGTTTGT  AAAGAAAAAA
1001  GCGCGTGGA  TACGATTATT  TGGTTTGCG  CATTGATTAT  GATGGCCGCA
1051  TTTTAAATA  AACTCGGACT  GATTAAATGG  TTCTCCGGAG  TGTGGCGGA
1101  AAGTGTGGC  GGTGTTGGCG  TTAGCGGCAC  GGCTGCGGGC  GTAATCCTCG
1151  TGCTTGCTTA  TATGTATGCG  CATTATATGT  TTGCCAGTAC  TACTGCACAT
1201  ATTACCGCTA  TGTTCGGCGC  ATTTTTCGCT  GCTGCCGTTT  CACTGAATGC
1251  CCCGGCGATG  CCGACCGCGC  TGATGATGGC  GGCCGCATCT  AACATTATGA
1301  TGACCTCAC  TCATTATGCG  ACCGGTACTT  CGCCTGTGAT  TTTCCGTTCC
1351  GGCTACACCA  CAATGGGAGA  ATGGTGAAG  GCGGGTTTTA  TCATGAGCGT
1401  AGTCAATTTT  CTGATTTTTT  TCGTTATCGG  CAGCATTGTT  TGGAAAGTTC
1451  TGGGGTATTG  GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```
a929.pep
  1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
 51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*
```

m929/a929 99.6% identity in 487 aa overlap

	10	20	30	40	50	60
m929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFIGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
m929.pep	70	80	90	100	110	120
	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
a929	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
m929.pep	130	140	150	160	170	180
	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
a929	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
m929.pep	190	200	210	220	230	240
	LALVNYHNSPISAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
a929	LALVNYHNSPISAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240
m929.pep	250	260	270	280	290	300
	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
a929	PLILYFLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
m929.pep	310	320	330	340	350	360
	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
m929.pep	370	380	390	400	410	420
	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAVSLNAPAM					
a929	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
m929.pep	430	440	450	460	470	480
	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					

a929 WKVLGYWX

g930.seq not found yet
g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

```
m930.seq
1  ATGAAACTTC CTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAATGGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

```
m930.pep
1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QODIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLVEGEHHA
101 RFQFALKRAL RETGFOAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

```
g930-1.seq (partial)
1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCCGTAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCGAGG
201 ACGTATTGCA GCATTCCAAA ACAAAATTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCT GTAGAGAGAG AACCAGAACCA
351 AAGTGATGTC GTGGTGCAAT GCGGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTCTTA
501 TGTAAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTCCGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTTCGGC TTCAAACGCC TGTGTATCGG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACAGGGGAAA CAAAAGTTA
801 CATTGATGAT GCCGAACGTA CTGTACAACG GCGTAAACCC ACAGGTGGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCGATAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TGGCGCGGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTGCGCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATTCGGG CCAAACCTTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAGAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGTTATTTC GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

```
g930-1.pep (partial)
1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMNDS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSLGSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FEGGTSRMKI WTASADVNTF FOIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD
```

451 IFTGRALKKP EYFQTKKWT GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```
1 ATGAACTTC CTTATCCTA TTGCTTAAT ATTCGCTTTT TGTCTTGGTG
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAC GAAGTGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTCGA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAAAC
701 AAGTGTATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATAAT TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAAGTTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA AAAAAAGTT
1151 ACATTGATGA TGCCGAACAT ACTGTACAAC GCGTAAAAC TGCGGGTTGG
1201 TTGGCAGAAC TTTCCACAA AGAATATATC GGTGCGAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAACGCGC GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAAC CTTTGGCGAA GGCACGTCAC GTATGAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTCAAATC GGTAAACAGC TATTTGCCA
1401 TGACCATATC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACTGGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACCGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTAAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTCAGGACA ATCCGCCAAA TGTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACCGGGGCA GATAAAGCTT GCGCGCAACC TGCAATACGA
1701 TATATTACG GCGCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```
1 MKLPLSYLPN IRFLSWCCLL AGIAPATLL ASPNPAEIRM QQDIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFG NKFPTRSNDL
201 LNLRLDLEQL ENLKLRLTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DCHRRKEGGS NYAVHYSAPF GKWTWAFNHN GYRYHQAQVS LSEVYDYNKG
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKSYYIDAEI TVQRRKTAGW
401 LAELSHKEYI GRSTADFLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWI WRNDLSWQFK PGHQLYLQAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFG VGYTF*
```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEHHARFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI					
g930-1.pep	GKCLHAGDINQIMSLAQNALIGRGYTTTRI					
				10	20	30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQTLIPSYLRSIRIDRSNDDQTHAGRIAAFGNKFPTRSNDLLNLRDLE					
g930-1.pep	LAAPQDLNSGKLQTLMPGYLRSIRIDRSNDDQTHAGRIAAFGNKFPTRSNDLLNLRDLE					
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLENLKRLPTAEADLQIVPEGEFPNQSDVVVQWRQRLPYRVSVGMDSNGSEATGKYQG					

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```

g930-1.pep  QGLENLKLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150

m930-1.pep  270      280      290      300      310      320
NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210

m930-1.pep  330      340      350      360      370      380
NHNGYRYHQAVSGLSEVYDNGKSYNTDFGFNRLLYRDAKRKTYLGVKLWMRETKSYIDD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NHNGYRYHQAVSGLSEVYDNGKSYNTDFGFNRLLYRDAKRKTYLSVKLWLTRETKSYIDD
              220      230      240      250      260      270

m930-1.pep  390      400      410      420      430      440
AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALARAPEEAFGEGTSRMKI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  AELTVQRRKTGWLAEASHKGYIGRSTADFKLKYKHGTGMKDALARAPEEAFGEGTSRMKI
              280      290      300      310      320      330

m930-1.pep  450      460      470      480      490      500
WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSDQKLAIGGHHTVRGFDGEMSLSAER
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSDQKLAIGGHHTVRGFDGEMSLPAER
              340      350      360      370      380      390

m930-1.pep  510      520      530      540      550      560
GWYWRNDLSWQFKPGHQLYLGADVGHVSGSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGSAKWLSGQTLACTAGIRGQIKLGGNLHYD
              400      410      420      430      440      450

m930-1.pep  570      580      590
IFTGRALKKPEFFQSRKWASGFQVGYTF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  IFTGRALKKPEYFQTKKWTGFGVGSFX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAAAACCG ACAATACGGC TACACCGTT TCGGCAGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2859>:

```
m931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACGACACCG TTTTCCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```
m931.pep..
1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
g931.pep	70	80	90	100	110	120
	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
	: :					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	130	140	150	160	170	180
	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNVVPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

```
a931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAATACGA TTTTCCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
```

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451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VFPQPVKIRR VVVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVQPVKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTT
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCAATCCC TATCCGGGAT CAGCCTCGGC GGCATTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAGG CTGGTGTCGT AAGGTTTCG ACCCTTATCC CGAAAACAAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWR KGFDPYPENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTGC CACTCACCGC

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```

51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTGAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCGCTC GCGCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GGCGCGTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGGGCATT GTTATGTTGC CGTTTGATT TCAGACGGCA
651 TTTTGTTC AAGCGTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1 MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51 LTPEAVKDTI PAQAQANGNN GQPVTKRRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPOCA HQQGFHAQP
151 PKTTGGAGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLLGALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1 ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51 ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCG TGCCGAAGCA CAGGCAAACG GCAACAACgG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCCTGGTC GGCGCGGCGG CAGGCGCGTT TATCGGCAAC
251 GCCTGCGCAA ACAAATTCAC ACGGGCAGGC AACCAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGCAGCCT ACCATCAGTC CGCAGCCCCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACGCGCG
451 CCCCCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCGG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTtT GCATTGTGA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1 ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51 TGXRRAAVYL RPIDRKLAAA KPGRRGGRRV YRQAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQQG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

```

m934.pep          10      20      30
                  RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                  |||:|||
g934              10      20      30      40      50      60
                  MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI

m934.pep          40      50      60      70      80      90
                  PAEAQANGNNGQPVTKGRRRAAVYLRPIDRKLAAAKPGRRGGRVYRQAGKQIHTGROPR
                  |||:|||
g934              70      80      90      100     110     120
                  PAQAQANGNNGQPVTKGRRRAAVYLRPIDRKLAAAKPDWRGGRRVYRQAGKQIHTGGQPR

                  100     110     120     130     140     150

```

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTGC CACTCGCCGC
51  TCGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AAACATTAGT
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGT CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG. TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGCGTGTGT CAAAGCCTGG TCGGCGCGCG
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTG ACACGGGCGA
351 GCAACCAAGA CAGTCCCGTC GCCCGGCGCG CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCAGA CGGTTACCGC CCGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TCGCGGTTTC CGGCAGAAGG
551 CGGTAAATCC GGCGTGCCAA TGCCGTGTGA AGGGCTTTCA GACGGCATT
601 TTGTATTGTT TAGGGACATT GTTATTGTTG CGTTTGATT TTAGACGGCA
651 TTTTGTTC AAGAGTTTGA TGTGGGATG CGAATTCTGA

```

a934.pep

1	<u>MKKIIASALI</u>	<u>ATFALAACQD</u>	DAQARLEQQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAEQANGNN	GQVPTX*RR	AVYLRPTDRK	LAAAKPGRRG
101	GRRVYRQRG	KQIHTRGRQ	QSRRPARACR	LPSVRTSQCA	HQQGFHAQP
151	PCKTTGGAGA	ALPDNAPAR	QLPMPRHARF	RQKAVNPACQ	CRLKGFQT <u>AF</u>
201	LYLLGTLLCC	RLIFRRHFVS	KSLMSGWOF*		

```

m934.pep      10          20          30
               RLEQQQKQIEALQQQLAQQAADTVYQLTPEAVKDTI
               |||||
a934          MKKIIASALIATFALAACQDDAARLEQQQKQIEALQQQLAQQAADTVYQLTPEAVKDTI
               10          20          30          40          50          60

               40          50          60          70          80          90
m934.pep      PAEAQANGNNGQPVTGXRRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
               |||||
a934          PAEAQANGNNGQPVTXXRRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
               70          80          90          100         110         120

               100         110         120         130         140         150
m934.pep      QSRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRLPPPPRYARF
               |||||
a934          QSRRPARACRLPSVRTSQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPHRHF
               130         140         150         160         170         180

               160         170         180         190         200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
               ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a934          RQKAVNPACQCRLKGFQTAFLYLLGTLCCRLIFRRHFVSKSLMSGWQFX
               190         200         210         220         230

```

g935.seq not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GGCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAATC
801 AGCTTATGAC GACGGGTTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CGGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTTCG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGTTGGGC
1201 GGCAGCGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGGCTG
1251 GGCAGGAGAG TGGCGGCGAG TGGGCGGTTT GAACAGTCGG GTTTCGCGCT
1301 CTTATGCCCC CCGCAACTAT AAGGGCGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDAKTK RVNNRRLPPY MLAGHVGVL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

m935.pep	10	20	30	40	50	60
	MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
a935	MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
	10	20	30	40	50	60
m935.pep	70	80	90	100	110	120
	DGDFFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	130	140	150	160	170	180
	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	190	200	210	220	230	240
	RKKTEGLTGWRFGSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFGSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
m935.pep	250	260	270	280	290	300
	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1 ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51 TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTTCG CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTC CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCGGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTT CGGAAAAAAA
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCGGGCGGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GCGGAAAAAG CTGACGCCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC AGTAAAAATC
801 AGCTTATGAT GACGGGTTCG GCAGGGCGTA TTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTTAT GTTTCGTTCG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGGTTG
1251 GGCGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1 MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVENDAPRV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVERYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRONGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDAKTK RVNRRRLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFSV
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1 ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51 TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTTCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTC CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCGGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCCGTTT TGGAAAATGT GGGGCGTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGVAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNPYAKRRNSEVFVSADWRFK					
a935	GRTESNPYAKRRNSEVFVSADWRFK					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGCGCTGCT TCAGCGCAGT CGTCGCGGG GCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGCGGAC ATCGCCGGCG
401 ACACCTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACcgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVS AVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```

1351

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng)

from *N. gonorrhoeae*:

m936/g936

	10	20	30	40	50	60
m936 . pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSVD RRTTGAQTDDNVMALRIETT					
	: : : : :					
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAGAKSVID RRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936 . pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	: : : : :					
g936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130					
m936 . pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936 . seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CCGTCCTCAG
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGC	GCGGCGGTCTG
101	GCGCGAAATC	CGCCGTCGAC	CGCCGAACCA	CCGGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCACC	GCCGCTCCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTCGGCTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAAACAG
301	TTCGTCGGTC	AGATTGCACG	TTCCGAACAG	GCCGCGGAAG	GCGTGTACAA
351	CTACATTACC	GTCGCCTCCC	TGCCGCGCAC	TGCCGGCGAC	ATCGCCGGCG
401	ACACTTGGA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACCTACGT
501	TATGGGCATC	CTCACCCCG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCGT	CGGCGTACAA	AAAGTCATCA	CCCTCTACCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936 . pep

1	MKPKPHTVRT	LTAAVLSLAL	GGCVSAVVG	AAVGAKSVD	RRTTGAQTDD
51	NVMALRIETT	ARSYLQNNQ	TKGYTPQISV	VGYNRHLLLL	GQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	QR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936 . pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSVD RRTTGAQTDDNVMALRIETT					
	: : : : :					
a936	MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGAKSAVD RRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936 . pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	: : : : :					
a936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120

m936 . pep VASLPRTA

1352

a936 |||||
 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
 130 140 150 160 170 180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCGTCCTCAG
51  CCTTGCCCTC  GCGCGCTGCT  TCAGCGCAGT  CGTCGGCGGG  GCCGCCGTCG
101 GCGCAAAATC  CGTCATCGAC  CGcgcAACCA  CCGgcgcgca  AACCGATGac
151 aACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ACCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCCGCGAAG  GCGTATACAA
351 CTACATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCGGGCGAC  ATCGCCGGCG
401 ACAC TTGAA  CACGTCCAAA  GTCCGCGCca  cgcTGTGGG  CATCAGCCCC
451 GCTACACAGG  CGCGCGTCAA  AATCATTACC  TACGGCAATG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCaccgT  CGGCGTACAA  AAAGTCATTA  CCCTCTACCA  AAACCTACGT
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1  MKPKPHTVRT  LIAAVLSLAL  GGCFSAVVGG  AAVGAKSVID  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIT  YGNVTYVMGI  LTFEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201 QR*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCATTTTCAG
51  CCTTGCCCTT  AGCGGCTGCG  TCAGCGCAGT  AATCGGAAGC  GCCGCCGTCG
101 GCGCGAAATC  CGCCGTCGAC  CGCCGAACCA  CCGCGCGCA  AACCGACGAC
151 AACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ATCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCCGCGAAG  GCGTGTACAA
351 CTATATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCCGGCGAC  ATCGCCGGCG
401 ACAC TTGAA  CACATCCAAA  GTCCGCGCCA  CGCTGTTGGG  CATCAGCCCC
451 GCCACACAGG  CGCGCGTCAA  AATCGTTACC  TACGGCAACG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCACCGT  CGGCGTACAA  AAAGTCATCA  CCCTCTACCA  AAACCTACGT
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1  MKPKPHTVRT  LIAAIFSLAL  SGCVSAVIGS  AAVGAKSAVD  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIV  YGNVTYVMGI  LTFEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201 QR*
  
```

m936-1/g936-1 95.5% identity in 202 aa overlap

	10	20	30	40	50	60
m936-1.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
g936-1	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAASVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936-1.pep	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					
g936-1	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGCGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTGCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCACGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGGTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGA CACATCCAAA GTCCGCGCCA CGTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTA AVLSLAL GGC VSAVVG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMI LTPEEQAQIT QKVSTTVGVQ KVTILYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT
              |||||
a936-1      MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGAKSAVDRRTTGAQTDDNVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTAgt ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAAT
101 GGAAactGGA AACTTccett acctacctgA acaGCGAAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGA CTGAccg GCAataccgA CATTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACCTCGacg GCAACGGCAA

```


1354

```

351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
401 TCCTtaAAGa cgGCAAAAAT CCCGCACTCA TCGCTTTCCT CGAAAGCACG
451 GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCGGGAAAAT CGTGGCTCAT
501 CGGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCCTT TCCCTCACC
551 CCGCCTACCG CATCAACGGC AGCAAAACCC TTTTACAGCA CGTCAAATAC
601 AAAGCAGGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
651 CGACAGAATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCG
701 ACCGCATAGA CGGCAAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
751 CATTTCGGCG CAGGTTTCGG TTTTACCAAA ACCGCGGCTT TAAACGCATC
801 CGCAGTTTC AACGTTTCAG GGCAAAGCAG TTCCGAACTG AAATTGGGCG
851 TACAGCATAC ATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:

g937.pep

```

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETS TYLNSENSRA
51 ALASPVIYQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIY
101 SSGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
151 VYEKSRNKAS SGKSWLIGAT TYKAIDPIVL SLTAAYRING SKTLSDDVKY
201 KAGNYWMLNP NISFAANDRI SLTGGIQWLG KQPDRIKGGK ESARNTSTYA
251 HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVOHTF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

```

1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGCGCGCA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAgAAAaCGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCGCCCC TAATCAGCTT TCTTGAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCAACATCT CATTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pep..

```

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNRR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTND DMLVGTGLRL YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVOHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10      20      30      40      50      59
g937.pep  MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETS LTYLNSENSRAALASPVIYQ
          || || : : : || : : ||||| : ||||| : ||||| : || : |||
m937      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETS LTYLNSENNRAELAAPVYIQ
          10      20      30      40      50      60
          60      70      80      90      100     110     119
g937.pep  TGSASFIPVPTTEIQENGSTNDMLAGTLGLRYGLTGNTDIYSGSGSYLWHEERKLDGNGKTR

```

a937.seq

a937 . pep

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	:					
a937	MKRIFLPALPAILPLSAYADPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m937.pep	TGATSFIPIPTEIQENGSTNDMLVGTGLGLRYGLTGNTDIYGGSGSYLWHEERKLDGNSKTR					
	:					
a937	TGATSFIPIPTEIQENGSTNDMLVGTGLGLRYGLTGNTDIYGGSGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKKTALNASARFNVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLFAV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTACGATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAA AATACCATCA
551 TGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTGAA AGCGGTCGGC
601 AACTTTATCC AAGGTTTGGC TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLFAV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTHGSAV MKPVVMNLS QDILNVSAFY
101 AKQPKSGEA NPENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVEQ MNAYKSGQRK NTIMEDIANR MSEDILKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLFAVLAAGAVSASP KADVEKGQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					
a939	MKRLTLFAVLAAGAVSASP KADVEKGQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					

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```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNAP
              |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVMNLSQDILNVSAFYAKQQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGGT GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGCTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQGSAGSCGASKSAEGSCGASKSAEG
              10      20      30      40      50      60

              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |||||
g950          SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGCTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

```

      10      20      30      40      50      60
a950.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          |||
m950      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          |||
      70      80      90     100
a950.pep  EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||
m950      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
          |||
      70      80      90     100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTT ACGCTGTTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTTGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGGGC GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TCGGAACGTT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTTGGAA GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGCT GCTGGTGCAA GCGCCGTGTC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCC CCGTGCAGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTTCCG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAAATA TTGCCCCCA CTTTAATGAC GTTGCTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAATTT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGAA CGTGCTGTTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTTGA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACCTTC GGCAGCGGGA
1351 AGCAGCGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCGGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAATC AACCAGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCCAT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTTGACGTA TGGACGACG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GGCGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GQAYAAGAAD VELPKVEGVK LRKHRRYSEE
```

```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHL DGLE EVLAQSDDVQ KRRIFLLLVQ AAVQQGGVAQ KASKAVRRRAA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQTDTQN LSAVWQEMEI MNLVSLRKP DAYARLNVLL
301 EHNPNANLYI QAAILAA NRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLK KVS APEYLFDKGV LAAAAAELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALS KLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYLGKD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1  ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51  CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTTC AAGAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCGGCAG TGGCGGAGCG
201 GGTAAATCAG ATATTTACGT TGCTGGGAGG GGAACCGGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCGGA ACGGCCTTG GAAATGGCGG TGTCGCTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGAGG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGCGGACGAA GGACAGAACC GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGGCGTTGA AATATGAACA TCTGCCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGGACGCG AAAAGGAAA GGAATCGGA GCTTTCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCACCTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCCGAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTT CGGCCGCTG GCAGGAATG GAAATTATGA
851 ATCTGTTTC CCTGCACAGG CTGGATGATG CCTATGCGG TTTGAACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GCGGCGAAAG CAAAAGAAG GTGCTTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACCG CAGGGGACG GAGGAACAG GGAGCAGGGC GGCCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
1201 ATCGGCAGGG TGCGGAAACT TCCGAACAG CAGGGCGGCT ATTTACGGC
1251 AGACAATTG TCCAAAATAC AGATGCTCGC CCTGTCGAAG CTGCCCGATA
1301 AACGCGAGGC TTTGAGGGG TTGGACAAGA TTATCGAAA ACCGCTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGTACAGC GGTCAAGTGT
1401 TTACGATCGG CTTGGCAGC GGAATAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATAC CAAATCAACC CGGACGATAC CGCTGCAAC GACAGCATAG
1601 GCTGGCGGTA TTACCTGAAA GCGACGCGG AAAGCGCGCT GCCGTATCTG
1651 CGGTATTCTG TTGAAAACGA CCGGAGGCC GAAGTTGCCG CCCATTGGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAACGCTC
1801 AACGTCACG GCATCGCATT GCCCAACCT TCCGAAAAC CTCGGAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1  MIMLPNRFKM LTVLTATLIA QVSAAGGGA GDMQKPEVG KVFRKQQRYS
51  EEEIKNERAR LAAVGERVNO IFTLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHL DGL LEEVLAQADE QNRRVFLLL AQAQVQDGL AQKASKAVRR
201 AALKYEHLPE AAVADVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLTKYPEI LDGFFEQTDT QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAAILAA RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YAKVRQWLK VSAPEYLFDK GVLAAAAAVE LDGGRALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LDKREALRG LDKIIEKPPA
451 GSNTLQAEA LVQSVVYDR LGKRKMSD LERAFRLAPD NAQIMNNLGY
501 SLTDSKRLD EGFALLQTAY QINPDDTAVN DSIWAYYLGK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRTEL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVGVFRKQRYSEEEIKNERAR					
g951	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGVLRKHRRYSEEEIKNERAR					
	10	20	30	40	50	
m951.pep	70	80	90	100	110	120
	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
	60	70	80	90	100	110
m951.pep	130	140	150	160	170	180
	QAEMIIYQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLGLEEVLAQADEGNRRVFLLL					
g951	QAEMIIYQKWRQIEPIPGEAQKRAGWLRNVLRERGNQHLGLEEVLAQSDDVQKRRIIFLL					
	120	130	140	150	160	170
m951.pep	190	200	210	220	230	240
	AQAAVQODGLAQKASKAVRRAALKYEHLPAAVADVVFVSGREKEKAIGALQRLAKLDT					
g951	VQAAVQGGVQAQKASKAVRRAALKYEHLPAAVADVVFVSGREKEKAIEALQRLAKLDT					
	180	190	200	210	220	230
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVQEMEIMNLVSLHRLDDAYARLNV					
g951	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVQEMEIMNLVSLRKPDDAYARLNV					
	240	250	260	270	280	290
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEEQSRRAALTAAMMYADRRD					
g951	LLEHNPNANLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRRAAMTAAMIYADRRD					
	300	310	320	330	340	350
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL					
g951	YAKVRQWLKKVSAPEYLFDKGVLA AAAA AELDGGRAALRQIGRVRKLPEQQGRYFTADNL					
	360	370	380	390	400	410
m951.pep	430	440	450	460	470	480
	SKIQLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQSRVVYDRLGKRRKMISD					
g951	SKIQLALSKLPDKREALIGLNNIIAKLSAAGSTEPLAEALQRSIIYEQFGKRGKMIAD					
	420	430	440	450	460	470
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNNGYSLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	LETALKLTPDNAQIMNNGYSLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
	480	490	500	510	520	530
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQA AHLTGDKKI WRETL					
g951	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQA AHLTGDKKI WRETL					
	540	550	560	570	580	590
m951.pep	610					
	KRHGIALPQPSRKPRK					
g951	KRYGIALPEPSRKPRKX					
	600	610				

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*:

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep    MLPARFTTILSVLAAALLAGQAYAG--AADAKPPKEVGKVFRRQQRYSEEEIKNERAR
           ||| :||:||||:|:||: ||| |:| | ||||| ||||| ||||| |||||
m951        MIMLPNRFKMLTVLTATLIAGQVSAAGGGADMKPKPEVGKVFRRQQRYSEEEIKNERAR
              10      20      30      40      50      60
a951.pep    LAAVGERVNVQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSINAFE
             60      70      80      90     100     110

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m951      |||||
          LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
          70      80      90      100     110     120

a951.pep  120      130      140      150      160      170
          QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          |||||

m951      120      130      140      150      160      170      180
          QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          |||||

a951.pep  180      190      200      210      220      230
          AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
          |||||

m951      180      190      200      210      220      230      240
          AQAAVQQDGLAQKASKAVRRAALKYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
          |||||

a951.pep  240      250      260      270      280      290
          EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV
          |||||

m951      240      250      260      270      280      290      300
          EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV
          |||||

a951.pep  300      310      320      330      340      350
          LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
          |||||

m951      300      310      320      330      340      350      360
          LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
          |||||

a951.pep  360      370      380      390      400      410
          YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQQGRYFTADNL
          |||||

m951      360      370      380      390      400      410      420
          YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQQGRYFTADNL
          |||||

a951.pep  420      430      440      450      460      470
          SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
          |||||

m951      420      430      440      450      460      470      480
          SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
          |||||

a951.pep  480      490      500      510      520      530
          LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQATAYQINPDDTAVNDSIGWAYYLK
          |||||

m951      480      490      500      510      520      530      540
          LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQATAYQINPDDTAVNDSIGWAYYLK
          |||||

a951.pep  540      550      560      570      580      590
          GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          |||||

m951      540      550      560      570      580      590      600
          GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          |||||

a951.pep  600      610
          KRHGIALPQPSRKPRK
          |||||

m951      600      610
          KRHGIALPQPSRKPRK
          |||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1  ..TTGTCTTATC GTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTGTG
51  TTACGGAAAA ATCAAATGCG AGAGTTGGAA AGCGCGGCGG GATTTCATA
101 TTGTAAAGCA GGATTGGAT TTTTCTGCG GGGCGGCTTC GGTGGCGACG
151 CTTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTGGA
201 AAAACTGGGT AAGGAACAGA TCGCGCGGTC GTTTGAGGAT ATGCGGCGCA
251 TTATGCCCGA TTTGGGTTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301 CAGCTCGCGC AGTTGAAAAT CCCCGTCATC GTGTATCTGA AATACCGCAA
351 AGACGACCAT TTTTCGGTAT TCGCGGGAGT GGATGGCAAT ACGGTTTTGC
401 TTGCCGACCC GTCGCCGGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTTG
451 GAGGCTTGGC AAACCCGTGA GGGAAATTTG GCAGGCAAAA TTTTGGCGGT
501 CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551 ATCCCAAGCG GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGGCGT

```

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)
 1 ..LSYRLNAAPM FNDNPVVYVK IKLQSWKARR DENIVKQDLD FSCGAASVAT
 51 LLNNFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPDLGF EAKGYALSFE
 101 QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPSPG HVMSMSRAQFL
 151 EAWQTREGNL AGKILAVVPK KAEAISNKL FTHHPKQTE FAVGQVKWWR
 201 AY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq
 1 ATGATGAAGT TCAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT
 51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
 101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGCGGGA TTTCAATATT
 151 GTAAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
 201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
 251 AGCTGGATAA GGAGCAGATG CGCGCTCGT TTAGGATAT GCGGCGCATT
 301 ATGCGTGATT TGGGTTTGA GCGGAAGGCG TATGCCCTGT CTTTCGAGCA
 351 GCTCGCGCAG TTGAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
 401 ACGACCATT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
 451 GCCGACCCGT CGCTGGGGCA TGTTCATATG AGCAGGGCGC AGTTTTTGGA
 501 TGCTTGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
 551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
 601 CCAAAACGGC AGACGGAGT TACAGTCGGA CAAATCAGGC AAGCACGTGC
 651 AGAGTAA

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep
 1 MMKFKEYVLL ACVVVLSYR LNAAPMFNDN PVVYVKIKVQ SWKARRDFNI
 51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKLDKEQM RASFEDMRR
 101 MPDLGFCAK YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
 151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTQH
 201 PKRQTEFTVG QIRQARAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952: 92.5% identity in 201 aa overlap

		10	20	30	40	
g952.pep		LSYRLNAAPMFNDNPVVYVKIKLQSWKARRDFNIVKQDLDFSCG				
m952						
	10	20	30	40	50	60
	50	60	70	80	90	100
g952.pep	AASVATLLNNFYGQKLTEEEVLEKLGKEQMRASFEDMRRIMPDLGFCAKGYALSFEQLAQ					
m952						
	70	80	90	100	110	120
	110	120	130	140	150	160
g952.pep	LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPSPGHVMSMSRAQFLAWQTREGNLAGKI					
m952						
	130	140	150	160	170	180
	170	180	190	200		
g952.pep	LAVVPKKAETISNKLFFTTHHPKQTEFAVGQVKWWRAYX					
m952						
	190	200	210			
	LAVIPKKAETISNKLFFTQHPRQTEFTVGQIRQARAE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq
 1 ATGATGAAGT TCAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT

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```

51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTGTGTT
101  ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGCGGGA TTTCAATATT
151  GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201  TTTGAACAAT TTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251  AGCTGGATAA GGAGCAGATG CGCGCTCGT TTGAGGATAT GCGGCGCATT
301  ATGCCAGATT TGGGTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351  GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401  ATGATCATT CTGCGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451  GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501  TGCTTGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
551  TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTT CACACATCAT
601  CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651  AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1   MMKFYVFL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLNKLDKEQM RASFEDMRRRI
101 MPDLGFCAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

```

a952/m952    97.7% identity in 218 aa overlap

          10      20      30      40      50      60
a952.pep  MMKFYVFLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG
          |||
m952       MMKFYVFLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG
          10      20      30      40      50      60

          70      80      90      100     110     120
a952.pep  AASVATLLNNFYGQTLTEEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
          |||
m952       AASVATLLNNFYGQTLTEEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
          70      80      90      100     110     120

          130     140     150     160     170     180
a952.pep  LKIPVIVYLKRYKDDHFSVLRGIDGNTVLLADPSLGHVSMMSRAQFXDAWQTREGNLAGKI
          |||
m952       LKIPVIVYLKRYKDDHFSVLRGIDGNTVLLADPSLGHVSMMSRAQFLDAWQTREGNLAGKI
          130     140     150     160     170     180

          190     200     210     219
a952.pep  LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAE
          |||
m952       LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1   ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51  CTCGCCACAC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGGTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTT GCAACCCCTT ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACACA AATTCAACTT CAACGGCAAA AAAGTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCT CGTCAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

a953..seq

1	ATGAAAAAAA	TCATCATCGC	CGCGCTCGCA	GCAGCCGCCA	TCGGCACTGC
51	CTCCGCCGCC	ACCTACAAAG	TGGACGAATA	TCACGCCAAC	GCCCGTTTCT
101	CTATCGACCA	TTTCAACACC	AGCAACCAAC	TCGGCGGTTT	TAACGGTCTG
151	ACCGGTTCCG	TTGAGTTCGA	CAAGCAAAAA	CGCAGCGGTA	AAATCGCATAT
201	CACCATCCCC	GTTGCCAACC	TGCAAAGCGG	TTCCGAACAAC	TTTACCGACC
251	ACCTGAAATC	AGCCGACATC	TTGCAGTCGC	CCCAATATCC	GGACATCCGC
301	TTTGTTTCCA	ACCAATTCAA	CTTCAACGGC	AAAAAATCTG	TTTCGGTTGA

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```

351 CCGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GCGCACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
  1  MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
 51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
101  FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAKEFNICY SPMLKTEVCG
151  GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

```

a953/m953    97.3% identity in 187 aa overlap

          10      20      30      40      50      60
a953.pep  MKKIIIAALAAAIGTASAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m953      MKKIIIFAALAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK
          10      20      30      40      50      60

          70      80      90      100     110     120
a953.pep  RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m953      RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL
          70      80      90      100     110     120

          130     140     150     160     170     180
a953.pep  TMHGKTAPVKLKAKEFNICYSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m953      TMHGKTAPVKLKAKEFNICYSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
          130     140     150     160     170     180

a953.pep  QIEAAKQX
          |||||
m953      QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
  1  ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
 51  GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101  AATATCAATT TGCAGATGAG AACAGGCTT TTTATTTTGA ACGCGCGGCC
151  CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201  AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251  TTACTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301  TACCGCGTCT GCAAACAGGC TGCGCAAGAT GCAGAAATCC TGATGAAGAG
351  TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTAGAT AAGGAAAGTT
401  ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
451  GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
  1  MKKFYFVLLA LGLAACGQEQ SOKADAEQYF FANKYQFADE KOAFYFERAA
 51  RFRVLQQLGL GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP
101  YRVCKQAAQD AEILMKSMVT SGGGGTTDL D KESYQNYRKS MQECRKTITE
151  AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```
g957.seq (partial)
  1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCGTGT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCTGTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATCGGGGAAT TGATGCCCGG GGGGatgaag gcgaacagtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaattattatt tgaaaaacgg aaatcttttt
901 attgccaat cttcgacggt aaccttgaac acggatggcg taacggcgga
951 tatgcaaac tatcatgctc aacaaacgtt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```
g957.pep (partial)
  1 MFKKFKPVL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
 51 AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSU VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YENCLGCMYQ AQVYLAKYRD VANDEQKQWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGKM ANSLVVGYYDA DGLFPKQVWS VDNGKKPQSV EYILKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQOTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```
m957.seq
  1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCGTGT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAACT GTGGATGACG
251 GTCCTGTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CCGGGAAAAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGGAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAGCG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTTGGT GCGGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAAAAAT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```
m957.pep
  1 MFKKFKPVL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVKPNPNFV
 51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSU VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YENCLGCMYQ AQVYLAKYRD VANDEQKQWD FRKESNRIAS DSRNSVFYQN
```

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251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
 301 IAQSSSTVALK ADGVTADMOT YHAQQTWYLD GGRIIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVF	FWLGTGIAYEINPRWFL	SDTATEVPENPN	AFVAKLARLFRNA		
m957	MFKKFKPVLLSFFALVF	FWLGTGIAYEINPRWFL	SDTATEVPKPN	AFVAKLARLFRNA		
	10	20	30	40	50	60
	70	80	90	100	110	120
g957.pep	DRAVVIVKESMRTEESLAG	AVDDGPLQSEKDYLA	IRLSRLKEKAKWFHV	TEQEHGEEV		
m957	DRAVVIVKESIRTEENLAG	TVDDGPLQSEKDYLA	IRLSRLKEKAKWFHV	TEQEHGKEV		
	70	80	90	100	110	120
	130	140	150	160	170	180
g957.pep	WLDYYIGEGGLVAVSLS	QRSPEAFVNAEYLYR	NDRPFVSVNVYGGT	AHGENYETTGEYRVV		
m957	WLDYHIGEGGLVAVSLS	QRSPEAFVNAEYLYR	NDRPFVSVNVYGGT	VHGENYETTGEYRVV		
	130	140	150	160	170	180
	190	200	210	220	230	240
g957.pep	WQPDGSVFDAAAGRGK	IGEDVYEHCLGCIYQ	MAQVYLAKYRDVAN	DEQKQVWDFREESN	RIAS	
m957	WQPDGSVFDAAAGRGK	IGEDVYEHCLGCIYQ	MAQVYLAKYRDVAN	DEQKQVWDFRKESN	RIAS	
	190	200	210	220	230	240
	250	260	270	280	290	300
g957.pep	DSRDYVFYQNMRELM	PRGMKANSLVVG YD	ADGLPQKVYWSVDN	GKKPQSVEYYLKNG	NLF	
m957	DSRNVVFYQNMRELM	PRGMKANSLVVG YD	ADGLPQKVYWSFDN	GKKRQSF EYYLKNG	NLF	
	250	260	270	280	290	300
	310	320	330			
g957.pep	IAQSSSTVTLKTDGVT	ADMOTYHAQQTLYLDG				
m957	IAQSSSTVALKADGVT	ADMOTYHAQQTWYLD	GGRIIVREEKQGDRL	PDFPLNLENLEKEV	R	
	310	320	330	340	350	360
m957	YAEAAARRSGGRRDL	SHX				
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTTTG	CAC TTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCGGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCACGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

```

951 CTATCATGCG CAACAGACGT GGTATTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGCGCA GACGTTCGGG
1101 CGGCAGGCGC GACCTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKQRQSFYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA				
m957					
	10	20	30	40	50
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA				
	10	20	30	40	50
a957.pep	60	70	80	90	100
	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYALAVRLSRLKEKAKWFHVTEQEHGEEV				
m957					
	60	70	80	90	100
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYALAIRLSRLKEKAKWFHVTEQEHGKEV				
	70	80	90	100	110
a957.pep	120	130	140	150	160
	WLDYYIGEGGLVAVLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
m957					
	120	130	140	150	160
	WLDYHIGEGGLVAVLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
	130	140	150	160	170
a957.pep	180	190	200	210	220
	WQPDGVSVDASGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFREESNRIAS				
m957					
	180	190	200	210	220
	WQPDGVSVDAAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS				
	190	200	210	220	230
a957.pep	240	250	260	270	280
	DSRDSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFYYLKNGNLF				
m957					
	240	250	260	270	280
	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFYYLKNGNLF				
	250	260	270	280	290
a957.pep	300	310	320	330	340
	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR				
m957					
	300	310	320	330	340
	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR				
	310	320	330	340	350
a957.pep	360	370			
	YAEAAARRSGGRRDLSHX				
m957					
	YAEAAARRSGGRRDLSHX				
	360	370			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.oa
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCCGCCAG CATTGCGCCG CCGATACCGT TGCGGCGGAA GAGCGGCACG

```



```

101 GGCCTGTCTCG AGAAGGCGGT GCGCAGGCGC CGTCCGAATC CGCACAAGCT
151 TCCGATTTGA CCTCGGTTT GACCTGCCTG TTTTGCAGTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCAGAG CCGCCGTTCA AGGCAGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGGGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTCCGC CTCCAACAGG ACGGTACGCT GATTCTGGGG
451 GAAACCTGTA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACTG
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAAATC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCCGAT CCGGGAAAAG GCATAGGCGT TGCCAAACAC GCGCCTTCG
701 TGTTCCGGCG CGTTCCTCTT TCTTATACGC CTTGGGCGGA CTTCCCGCTT
751 GACGGCAACG GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGGCGTT TCCCTTTCCG TCCCTTATTA TTTCAACCTT GCCCCAACT
851 TCGATGCCAC TTTCCGCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGGACAAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCGA GCGGGCGGGA GGCAGCCTGA ATGCCGGCCT TTCGGTTCAG
1201 AAATACCAGA CGCTGGCAAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAATGGG ATTTCAGCAA
1401 CAGCTGGGCG TACGTCCGCC CAAACTCGG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCCGGCGG AAAGCATCCC GCAGCGTCGG GCGCGTTTG
1501 CCCGTTGTCA ATATCGACGG CGGCACAACC TTGAAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTTACAACT
1601 ATATTCTTGC CAAATCTCAA AACGACCTGC CCAATTTGTA TTCGTCGGAA
1651 AGCAGGTTCT GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCGGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTTCTAT TCAAGGATGA TCGGCTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTGCGCTCC GCGGGCATAG
1901 GCGGGCGGTT CACCTTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CCGCGCAGGC TACCGCCCCG CCCCCGAAA
2001 AGTGTGTAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAAATGG CGCTGACGCG CAACCTGTCT GCCGTCTGCC GCTACAACTA
2151 CGGTTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCGCTC TTTTTTTCAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCCGC AGGCAGGATG GATGTCGCGC
2351 TTCCCGGCTA CATCCCGGCC CACTCTCTTT CCGCCGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

```

g958.pep
1  LARLFLSKPL VLALGFCEGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51  SDLTLLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQQDGTILRG
151 ETLTYNLDQQ TGEAHNVME TEQGGRRLOS VSRTEMLGE GRYKLTETQF
201 NTCSAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRLP YSGQDGLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSHDGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
501 PVVNIDGGTT FERNTLFGG GVVQTIETPL FYNYPKSKS NDLNFDSSSE
551 SSFGYQQLFR ENLYYGNDR I NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSGVGNPR SRSDWAFAS GGIIGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLDADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAGRYV
751 TGENTYKNAV FFSLQLKDL S SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

```

m958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
51  CTTCGGCACG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA CGGTGTCCGA ACCCATACAG

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCAGAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAACCG
351 GACGACCCCTC AATACCGATT GGGCGGATTA CGACCAGTCG GCGGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGGGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAAACCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTCGAAGCC GATCGGGAAG AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGCGA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGACGGGC GTTTCCTTTT CCGTTCCTTA TTATTTCAC CTGCCCCCA
851 ATCTCGATGC CACGTTCCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCGG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCAGC ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC ACAAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTAGTGGCG CAGGCGGCGG GCGGCGAGCC TGAATGCCGG CTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTGC GCGTAAAAAC ACCGCGAGGG
1301 CGCAATCGG CGTGTCCGCA CAATTTACCC GATTACGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCTGGT CGTCTATCCC GACATCAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CTGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACCGCT CAGCCGCACT
1501 CTGCCCATTG TCAACATCGA CAGCGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTGCGC GGAGAAGTCC TGCAAACCTT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAACGACC TGCCCAATTT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAAGCC
1751 GTATTTTGA CGGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGCTCG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTGCGC TCCGGCAGCA
1901 TCGGCAGCCG CTTTATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAAGTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGTCTG AACGCCCGCT ACAATAACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAA ATGGCGCTGAC GCGCAACCTG TCGGCCGCTG TCCGTTACAA
2151 CTAGCGTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTTCGCG CTATATCACC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1  LARLFSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51  PLSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQODGTLIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGRRLO SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKIGIVAK HAAFFVGVPV IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VLSVPYYFN LAPNLDATEFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QTRFSDSR
451 ODGSRLLVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSR
501 LPIVNIDSGA TFERNTRMFG GEVLQTLFPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSVGKKP RNRSDWVAFS SGSIGSRFIL DSIHYNQND
651 KRAENYAVGA SYRPAQGVKL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAIEYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRKN
801  RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

m958/g958 89.3% identity in 802 aa overlap

	10	20	30	40	50	60
m958.pep	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
g958	LARLFSLKPLVLALGFCFGTHCAA-DTVAEEADGRVAEGGAQGASESAQASDLTLGSTC					
	10	20	30	40	50	
	70	80	90	100	110	120
m958.pep	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL					
g958	LFCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGQSKVKVRAEGSVIIERDGAVL					
	60	70	80	90	100	110
	130	140	150	160	170	180
m958.pep	NTDWADYDQSGDVTVTAGDRFALQQDGTLLIRGETLTYNLEQQTGEAHNVMEIEQGGRRLO					
g958	NTDWADYDQSGDVTVTGDRFALQQDGTLLIRGETLTYNLDQQTGEAHNVMEIEQGGRRLO					
	120	130	140	150	160	170
	190	200	210	220	230	240
m958.pep	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGIVAKHAAFFVGGVP					
g958	SVSRTAEMLGEGRYKLTETQFNTCSAGDAGWYVKAASVEADRGKIGIVAKHAAFFVGGVP					
	180	190	200	210	220	230
	250	260	270	280	290	300
m958.pep	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLVPPYYFNLPNLDATFAPSVIGERGAV					
g958	LFYTPWADFPLDGNRKSGLLVPSVSAGSDGVSLVPPYYFNLPNFDATFAPGIIGERGAT					
	240	250	260	270	280	290
	310	320	330	340	350	360
m958.pep	FDGQVRYLRPDYAGQSDLTWLPDHDKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
g958	FDGQIRYLRPDYSGQTDLTWLPDHDKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
	300	310	320	330	340	350
	370	380	390	400	410	420
m958.pep	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
g958	YYRDFYGGEEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM					
	360	370	380	390	400	410
	430	440	450	460	470	480
m958.pep	PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
g958	PRLSADWHKNAGRAQIGVSAQFTRFSHDGRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
	420	430	440	450	460	470
	490	500	510	520	530	540
m958.pep	ATYYSLNRFSGSEARRVSRTPPIVNIDSGATFERNTRMFGGEVLQTLERFLFYNIYIPAKS					
g958	ATYYSLDSFSGKASRSVGRVLPVNVNIDGGTTFERNTRLFGGGVVQTIEPRLFYNIYIPAKS					
	480	490	500	510	520	530
	550	560	570	580	590	600
m958.pep	QNDLPNFDSESSFGYQGLFRENLYYGNDRIANTANSLSAVQSRILDGATGEERFRAGIG					
g958	QNDLPNFDSESSFGYQGLFRENLYYGNDRIANAANSLSTAVQSRILDGATGEERFRAGIG					
	540	550	560	570	580	590
	610	620	630	640	650	660
m958.pep	QKFYFKDDAVMLDGSVGKKPRNSDWAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA					
g958	QKFYFKDDAVMLDGSVGKNPRSRDWAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA					
	600	610	620	630	640	650
	670	680	690	700	710	720
m958.pep	SYRPAQGGKVLNARYKYGRNEKIYLSKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
g958	GYRPAQGGKVLNARYKYGRNEKIYLAQDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
	660	670	680	690	700	710

	730	740	750	760	770	780
m958.pep	EAKKPIEVLAGEYKSSCGCWAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
g958	EAKKPIEVLAGEYKSSCGCWAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR					
	720	730	740	750	760	770

	790	800
m958.pep	MDVAVPGYITAHSLSAGRNRKP	
g958	MDVAVPGYIPAHSLSAGRNRKPX	
	780	790

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

a958.seq

```

1   TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCCGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACATATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATACAG
151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTGTGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCGCA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTGTCG AACGCAATCG
351 GACGACCTTC AATGCCGATT GGGCGGATTA CGACAGTCG GGCGACACCG
401 TTACCCGAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCGG
451 GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCTGTGTCGG CGGCGTTCCT ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTTCCTTTT CCGTTCCTTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCCGGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CTTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CTTGACCTGG CTGCGGCACG ACAAGAAAAG CGGCAGGAAT AACCCTATC
1001 AGGCGAAATG GCAGCACCAG CACGACATT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTCG ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGCGCGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAACCCGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAC ACCGCGAGGG
1301 CGCAATCGG CGTGTCCGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCCTCGT CGTCTATCCC GACATCAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCAAACT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTTCGG GCGCGAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTT CTGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGG
1801 CAGAAATCTC ACTTCAAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCCG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTCCGC TCCAGCGGCA
1901 TCGGCGAGCG CTTTATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAATACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGGTACGCG CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTGC
2351 CCGTTCGCG CTATATCCCC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CCGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

a958.pep

```

1   LARLFSLKPL VLALGFCEFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PLSLSLSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMERG
101 SQQVRAEGN VVVERNRTL NADWADYDQS GDTVTAGDRF ALQQDGLTLR
151 GETLTYNLEQ QTGEAHNVRM ETEHGRRRLQ SVSRTEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP

```

```

251 LDGNRKSGLL VPSLSAGSDG VLSVPPYYFN LAPNLDATFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLRNR VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSGVKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GA EYKSSCGC WGAGVYAQRV
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

	10	20	30	40	50	60
a958.pep	LARLFSLKPLVLALGFCGTHCAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC					
m958	LARLFSLKPLVLALGFCGTHCAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a958.pep	LFCSNESGSPERTEAAVQSGSEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL					
m958	LFCSNESGSPERTEAAVQSGSEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a958.pep	NADWADYDQSGDVTAGDRFALQQDGTLRGETLTYNLEQQTGEAHNVRMETEHGGRRLO					
m958	NTDWADYDQSGDVTAGDRFALQQDGTLRGETLTYNLEQQTGEAHNVMEIEQGGRRLO					
	130	140	150	160	170	180
	190	200	210	220	230	240
a958.pep	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGVAKHAAAFVFGGVP					
m958	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGVAKHAAAFVFGGVP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a958.pep	IFYTPWADFFLDGNRKSGLLVPSLSAGSDGVLSVPPYYFNLAPNLDATFAPGVIGERGAV					
m958	IFYTPWADFFLDGNRKSGLLVPSLSAGSDGVLSVPPYYFNLAPNLDATFAPSVIGERGAV					
	250	260	270	280	290	300
	310	320	330	340	350	360
a958.pep	FDGQVRYLRPDYAGQSDLTWLPDHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
m958	FDGQVRYLRPDYAGQSDLTWLPDHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a958.pep	YYRDFYGNKEIAGNVNLRNRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
m958	YYRDFYGNKEIAGNVNLRNRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
	370	380	390	400	410	420
	430	440	450	460	470	480
a958.pep	PRLSADWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
m958	PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
	430	440	450	460	470	480
	490	500	510	520	530	540
a958.pep	ATYYSLNRFSGQEARRVSRTLPIVNIDSGMTFERNTRMFGGVLQTLERLFFNYIPAKS					
m958	ATYYSLNRFSGQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLERLFFNYIPAKS					

1375

	490	500	510	520	530	540
	550	560	570	580	590	600
a958.pep	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANTANSLSAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANTANSLSAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a958.pep	QKFYFKNDVAVMLDGSVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKNDVAVMLDGSVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
	670	680	690	700	710	720
a958.pep	SYRPAQGVKNLARYKYGRNEKIYKSDGSYFYDKLSQLDLAQWPLTRNLSAVVRNYGFG					
m958	SYRPAQGVKNLARYKYGRNEKIYKSDGSYFYDKLSQLDLAQWPLTRNLSAVVRNYGFG					
	670	680	690	700	710	720
	730	740	750	760	770	780
a958.pep	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRVVTGENTYKNAVFFSLQKDLSSVGRNPADR					
m958	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRVVTGENTYKNAVFFSLQKDLSSVGRNPADR					
	730	740	750	760	770	780
	790	800				
a958.pep	MDVAVPGYIPAHSLSAGRNRKRF					
m958	MDVAVPGYITAHSLSAGRNRKRP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKISR
51  AQAEKAARAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MN	IK	HL	LL	TS	AA
g959	MN	IK	HL	LL	TS	AA

	70	80	90	100	109
m959.pep	VGG	KIT	DID	LE	HD
g959	VGG	KIT	DID	LE	HD

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1  ATGAACCTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCGGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

```

1  MNFKRLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51  AQAEEAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQ EYKVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MN	FK	RL	LL	TA	AA
m959	MN	IK	HL	LL	TS	AA

	70	80	90	100	109
a959.pep	VGG	KIT	DID	LE	HD
m959	VGG	KIT	DID	LE	HD

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51  TAAGCCCCCC TTGTTTGAAG CTCGCGGGCT CTTGCCGAGC TTCACCGACC
101 CCGTGTGCCC CAAGCTCTCT GCTCCGGCGG GGTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAGACCGA AATCGAAAAG CTGGCCAAAC AGCCCCAGTA
201 TGCCTATCTG AAACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAAACAGG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAAG
301 GCCGGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCCTT TGCCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGCGC ATGTCGGCAA AACCTGAAG GAACTGGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGTTGTAG CGGCGGCAAC GGCAGGCGTA TCCAACAAAC

```

```

551 TCGGTGCCTC TTCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTCAACGTTA ACCTGGCCAA TGGGGGCGT GCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCC AAAATCGCT CATGCCGTAG CCGGCTGTGC
801 GGTGTCAGCG GCGAATAAGG GCAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGCGG GAGGCTTTGG TTAATAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAACGCGG TAGAAAAATA TCGGTTTAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATTT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCTA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTATG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACG AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAATA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CATAAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAT TTAAGTTTGT
1551 TCTAATATAG GATGGTTCGC TTAACCAAT GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLIPS FTDPVVPKLS APGGYIVDIP
51 KGNLKTIEIK LAKQPEYAYL KQLQVAKNVN WNOVQLAYDK WDKQKEGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAFAFSL ASQASVSLIN
151 NKGDVKGTLK ELGRSRTVKV LVVAAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTTLFDETL
401 DWNDAKAVID IVVGTELNRA NKGEAAQVKV EVLEKNRPIY PNKGAVPNMS
451 TYMKNNPFGK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TCDRFYLDGQ
501 HKNHLEVFDE NGNEKFLVNM DGSLNQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTCC AGCCAAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAAAACAAC AAAACGTCGA TGCCAAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTTGCTGA AGAGACTAAG ACAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAAAC
651 AAACGTTCAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAAGCCG
701 AAGCTGCGGC TGGCAGAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCACAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GCGCTGTTCC AACCTTACAA CGTGGGTCGG TCAATGTAA CCGCTGCACT
951 CGCGGGCTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCCTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFPKAV LTTAILATFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

```



```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FN DIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKV KAAETAA GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAVGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet
a961.pep not found yet

g972.seq not found yet
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCG GATGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG CGGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAAA AGCAAATGGG TAAGGTTCCA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATCTCG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTGA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGA LK TXSKSSERMS EYEFYSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWFSTFHE DTLLKVS GCP LFSDAEYMYV LSRKLEELG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE D GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDI EIP LD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKKLNLTFF
301 HKLHYAKNAV GKLVNFMIE M GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKQYEYLS KVVHQNVDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

```

1379

```

251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTCGG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCG GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGCGG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAAAT CTCGTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTCTGT GGAGCTTTTC CAATTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAAATATG TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAA AGGCTTTTTC GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

a972.pep

```

1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKGKLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KNSRFRVRY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICKKFK NMPVPERFDQ RKKTLLNLTFE
301 HKLHYAKNAV GKLNVNMIEM GFDNSEIVES LKADSGFPGK LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLKTXSKSSERMSEVEYFSHFISDGKGKLEIPQRRGKQDGVFVDWISFTFHE					
a972	LTNRGGAKLKTNKSSERMSEVEYFSHFISDGKGKLEIPQRRGKQDGVFVDWISFTFHE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m972.pep	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
a972	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFFDGEYTPDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m972.pep	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDSGKTFYVGRKNSRFRVRYEKGRQLGDKE					
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDSGKTFYVGRKNSRFRVRYEKGRQLGDKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m972.pep	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICKKFKNMPVPERFDQ RKKKLNLTFE					
a972	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICKKFKNMPVPERFDQ RKKKLNLTFE					
	250	260	270	280	290	300

1380

	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPTYDVEKERKYQEYLSKVYHQNVVDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPTYDVEKERKYQEYLSKVYHQNVVDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTGCGC CTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCAAC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTGGGTACG GAatacggca gcgaagaagc cgacaccatc ggcggtTGG
701 TCATTcAGGA ATTGGGACAC CTGCCCCTGC GCGGCGAAAA AGTCCTTAtc
751 ggcgGTTTGC agttcaccgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQPHLKSIVL PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGGLVT FEDIIEQIVG DIEDEFEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEADTI GGLVIQELGH LPVRGEKVLI
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTAAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCAAC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTcm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

```

m973 . pep

1	MDGAQPKTNF	FERLIARLAR	EPDSAEDVLN	LLRQAHEQEV	FDADTLRLR
51	KVLDFSDLEV	RDAMITSRM	NVLKENDSIE	RITAYVIDTA	HSRFPVIGED
101	KDEVLGILHA	KOLLKYMFPN	EQFHLKSILR	PAVFVPEGKS	LTALLKEFRE
151	QRNHMAIVID	EYGGTSGLVT	FEDIEEQIVG	EIEDEFDEDD	SADNIHAVSS
201	ERWRIHAATE	IEDINTFFGT	EYSKEEADTI	GLGLVIQELG	LPVRGEKVL
251	GGLOFTVARA	DNRRLLHTLMA	TRVK*		

Homology with a predicted ORF from *N. gonorrhoeae*

m973/q973

		10	20	30	40	50	60
m973.pep		MDGAQPKTNFFERLIARLAREPDS	AEVDVNLNLRQAHEQEVFDADTLLRLEKVLDFSDLEV				
g973		MDGAQPKTNFFERLIARLAREPDS	AEVDVNLNLRQAHEQEVFDADTLTRLEKVLDFAELEV				
		10	20	30	40	50	60
		70	80	90	100	110	120
m973.pep		RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFPN					
g973		RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFPN					
		70	80	90	100	110	120
		130	140	150	160	170	180
m973.pep		EQFHLKSLIRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
g973		EQFHLKSVLRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
		130	140	150	160	170	180
		190	200	210	220	230	240
m973.pep		EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSKEEADTIGGLVIQELGH					
		:					
g973		DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFGTEYGSEEADTIGGLVIQELGH					
		190	200	210	220	230	240
		250	260	270			
m973.pep		LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973		LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
		250	260	270			

a973.seq

1	ATGGACGGCG	CACAACCGAA	AACAAATTTT	TTTGAACGCC	TGATTGCCCG
51	ACTCGCCCGC	GAACCCGATT	CCGCCGAAGA	CGTATTGACC	CTGTTGCGCC
101	AAGCGCACGA	ACAGGAACTA	TTTGATGCGG	ATACGCTTTT	AAGATTGGAA
151	AAAGTCCTCG	ATTTTCTCTA	TTTGGAAAGT	CGCGACGCGA	TGATTACCGC
201	CAGCGTATAG	AACGTTTTAA	AAGAANAACG	CAGCATCGAA	CGCATACCGC
251	CCTACGTTAT	CGATACCGCC	CATTGCGGCT	TCCCGCTCAT	CGGTGAAGAC
301	AAAGACGAAG	TTTTGGGTAT	TTTGCACGCC	AAAGACCTGC	TCAAAATATAT
351	GTTCAACCCC	GAGCAGTTCC	ACCTCAAATC	GATATTGCGC	CCTGCCGTCT
401	TCGTCCCCGA	AGGCAAATCG	CTGACCGCCC	TTTTAAAAGA	GTTCCGCGAA
451	CAGCGCAACC	ATATGGCAAT	CGTCATCGAC	GAATACGGCG	GCACGTCGGG
501	TTTGGTAACT	TTTGAAGACA	TCATCGAGCA	AATCGTCGGC	GACATCGAAG
551	ATGAGTTTGA	CGAAGACGAA	AGCGCGGACA	ACATCCAGCG	CGGTTTCGGC

1382

```

601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCCGGCAGC GAATACAGCA GCGAAGAAGC CGACACCATC GCGCGCCTGG
701 TCATTACAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GCGCGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
  51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLV FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
 201 ERWRIHAATE IEDINAFPGT EYSSEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

```

          10      20      30      40      50      60
m973.pep MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV
          |||
a973      MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV
          10      20      30      40      50      60

          70      80      90     100     110     120
m973.pep RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP
          |||
a973      RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP
          70      80      90     100     110     120

          130     140     150     160     170     180
m973.pep EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
          |||
a973      EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
          130     140     150     160     170     180

          190     200     210     220     230     240
m973.pep EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH
          :|||
a973      DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFPGTEYSSEADTIGGLVIQELGH
          190     200     210     220     230     240

          250     260     270
m973.pep LPVRGEKVLIGGLQFTVARADNRLHTLMATRVKX
          |||
a973      LPVRGEKVLIGGLQFTVARADNRLHTLMATRVKX
          250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTCCGCAC TCGCGCTGTC
  51 TGCCTGCGGC GGTCAGGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
 101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTGAATCT
 151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
 201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
 251 ACAGCCTTTT CCCCGCCTTG AACAAACGCG ATGCGGACGT TGTGATGTCG
 301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
 351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
 401 CTTCTTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
 451 CACACGGCGG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
 501 AATCGCGCGC TTGAAAAACG TCCCCCTGAT TATCAAAGAA CTGGAACACG
 551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
 601 AAAAAACAAC CGGCCAAAGG AATGGACTTC GTTACCTGCG CCGACTTCAC
 651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
 701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
 751 AAGATCTACG CCAAATATTT TGCCAAAGAG GCGGACAGG CTGCGAATA
 801 A

```

1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```
m981.pep
1  MKKWIAAALA CSALALSACG GQKDAAPA ANPGKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK NMNKGVVVTG
151 HTGDFSUSKL LGNDNPFIAR FENVPLIIKE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDV VTLDPFTTEH YGIAVRKGE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```
m981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGTGTCT
51  TGCCTGCGGC GGTACGGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
101 ACAAGTGTGA CCGCGTGGCT TCCAACGCGC AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTTA AACAAGGCGC ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCGGA AGATTTGAAA AACATGAACA AAGTCGCGCT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTGAAAAACG TTCCCTGAT TATCAAAGAA CTGAAAAACG
551 GCGGCTTGGT TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAAAACATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTACG CCAATATTTT TGCAAAGAA GACGGACAGG CCGCAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```
m981.pep
1  MKKWIAAALA CSALALSACG GQKDTAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK NMNKGVVVTG
151 YTGDFSUSKL LGNDNPFIAR FENVPLIIKE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDV VTLDPFTTEH YGIAVRKGE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKWIAAALACSALALSACGGQKDTA	PAANPDKVYRVASNAEFAPFESLDSKGNVEGF				
g981	MKKWIAAALACSALALSACGGQKDA	APAAANPGKVYRVASNAEFAPFESLDSKGNVEGF				
	70	80	90	100	110	120
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
	130	140	150	160	170	180
981.pep	ITQVVLVPGKGKVSSSEDLKNMNKGVVVTGYTGDFSUSKLLGNDNPFIARFENVPLIIKE					
g981	ITQVVLVPGKGKVSSSEDLKNMNKGVVVTGHTGDFSUSKLLGNDNPFIARFENVPLIIKE					
	190	200	210	220	230	240
981.pep	LENGGLDSVSDSAVIANVYKNNPAKGMDVTLDPFTTEHYGIAVRKGEATVKMLNDAL					
g981	LENGGLDSVSDSAVIANVYKNNPAKGMDVTLDPFTTEHYGIAVRKGEATVKMLNDAL					
	250	260				
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTGG AACACGGCG ATGCGGACGT TGTGATGTCG
301 GCGTAACCA TTACGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAATAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAGAA GACGGACAGG CCGCAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1  MKKWIAAALA CSALALSACG GQKDAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKISSSEDLK NMNKVGVTG
151 YTGDFSLSKL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIANV
201 KNNPTKGMDF VTLDPFTEH YGIAVRKGE ATVKMLNDAL KKVRESGEYD
251 KIKYKFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

m981.pep	10	20	30	40	50	60
	MKKWIAAALACSALALSACGGQKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQKDAAPAAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	70	80	90	100	110	120
	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	130	140	150	160	170	180
	ITQVVLVPKGKVVSSSEDLKNNMKVGVTGYTGDFSLSKLLGNDNPKIARFENVPLIIE					
a981	ITQVVLVPKGKISSSEDLKNNMKVGVTGYTGDFSLSKLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
m981.pep	190	200	210	220	230	240
	LENGGLDSVSDSAVIANVYKNNPAKGMDFVTLDPFTEHYGIAVRKGEATVKMLNDAL					
a981	LENGGLDSVSDSAVIANVYKNNPTKGMDFVTLDPFTEHYGIAVRKGEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	250	260				
	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

g982.seq

```

1 atcgcatcgc aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51 caacggcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgCgCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAacgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAaggca TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCCAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTT TTGCTGTTTC ACAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTT GGAACAAGTG GCGAAAGCCA GCCGCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGCG ACTTTGGTTC TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATttccGAAG Aagtcggcct GTCTTTGGA AAAgcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaaact ACCGTCATcg
1001 acgGCTTCGG CGACGcagc CAAatcgaag cgCGTGTGC CGAAATCCGC
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAAGTGGCAG GAGGCGTGGC AGTGATCAA GTCGGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAG ACCGCGTGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCTGC CAAAGTAAAC
1501 GTTCCGCGC TGCAACACGC CGCGTCTAtC GCCGCTGA GCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCGATA
1601 TGGGGGAAT GGGCGGTATG GCGGCATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

g982.pep

```

1 IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51 KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIIV
101 AEGMKYVTAG MNPTDLKRG I DKAAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYGDMIG MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGM GMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

m982.seq

```

1 ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51 AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAGAAGT TCGGTCCAAA ACCAACGACG
251 TGGCAGGCGA CCGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAA CAAATCGCTG CTTTGGACAA

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651	TCCGTTTGTA	TTGTTGTTG	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCCTGTTTT	GGAACAAGTG	GCAAAAAGCCA	GCCGTCCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGCGA	AGCCTTGGCG	ACTTTGGTGC	TGAACAACAT
801	CCGAGGCATC	CTGAAACCG	TGTCGCTCAA	AGCCCTGGC	CTCGGCACCC
851	GCCGCAAAAG	GATGTTGCAA	GATCATGCCA	TCTGACCCG	GCGCGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAAACC	ACCATCATCG
1001	ACGGCTTTG	CGACGCGACC	CAAATCGAAG	CGCGTGTTC	CGAAATCCCG
1051	CAACAAATCG	AAATCGCAAC	CAGCGATTAC	GACAAAGAAA	AATCGCAAGA
1101	GCGCGTGGCT	AAATTGCGAG	GCGCGCTGGC	AGTCATCAAA	GTCGGTGCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCGTGGA	AGACGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAGGC	GTGGTTCGAG	GCGGCGGCGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAGA	GCGAGGCGTA	CAATCTGTCT	TGCGCGCGCT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGGCGCG	GAACCCAGCT	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAG	GCAACTACGG	TTACAACGCT	GGCAGCGGCG
1451	AATACGCGGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGT	TGCAACACGC	CGCATCTATC	GCCGCGTTGA	TGCTGACCAC
1551	TGATTGTGATG	ATCGCTGAAA	TCCCAGAGA	CAACCCGCT	GTGCTGATA
1601	TGGGCGGCAT	GGGTGGTATG	GCGGCGATGA	TGTAA	

m982.seq

Homology with a predicted ORF from *N. gonorrhoeae*

mA982.pep

MAAKDVQFGNEVRQKMKVNGVNILANAVRVTLGPKGRNVVVVDRAFGGPHITKDGVTVAKEI

:|::||:| | ||||| | | :|:

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g982	IASQNLRFDNRFLOKMNNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALNLHTGNADQDAGVQIVLRVESPLRQIVANAGGEPVVVNKVLGKNGYGYNA
	430 440 450 460 470 480
g982	RARAALNLHTGNADQDAGVQIVLRVESPLRQIVANAGGEPVVVNKVLGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIGMGLDPKVTLSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
g982	GSGEYGDMIGMGLDPKVTLSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq

1	ATGGCAGCAA	AAGACGTACA	ATTCCGCAAT	GAAGTCCGCC	AAAAAATGGT
51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TGGGTCCCA
101	AAGGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TCGGCGGCCC	GCACATACC
151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAAGTGAAG	ACAAGTTGA
201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	CGCGTCCAAA	ACCAACGACG
251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCCGA	CCGACCTGAA
351	ACGCGGTATC	GACAAAGCCG	TCGCCGCTTT	GGTTGAAGAG	CTGAAAAACA

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```

401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCGG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGTACCTG
601 TCTCCTTACT TCATCAACGA TCGGAAAAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTG TTGCTGTTTCG ACAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAACCTGGCAG GCGCGGTGGC AGTAATCAAA GTCCGTGCCG
1151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGCGC
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CGCGTCTATC GCCGCGCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCATGA TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

a982.pep

```

1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLLENLDV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGDTV
301 ISEEVGLSLE KATLDDLQGA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSSEYGMIE MGVLDPAKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGM GGM*

```

m982/a982 99.3% identity in 544 aa overlap

	10	20	30	40	50	60
m982.pep	MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHIT KDGVTVAKEI					
a982	MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHIT KDGVTVAKEI					
	10	20	30	40	50	60
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSI VAEGMKYVTAG MNPTDLKRG I					
a982	ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSI VAEGMKYVTAG MNPTDLKRG I					
	70	80	90	100	110	120
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSI VAEGMKYVTAG MNPTDLKRG I					
a982	ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSI VAEGMKYVTAG MNPTDLKRG I					
	70	80	90	100	110	120
m982.pep	DKAVALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG					
a982	DKAVALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG					
	130	140	150	160	170	180
m982.pep	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFV LFDKKISNIRDLLPVLEQV					
a982	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFV LFDKKISNIRDLLPVLEQV					
	190	200	210	220	230	240
m982.pep	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFV LFDKKISNIRDLLPVLEQV					
a982	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFV LFDKKISNIRDLLPVLEQV					
	190	200	210	220	230	240

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	250	260	270	280	290	300
m982.pep	AKASRPLLI IAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLLI IAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY					
a982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA					
a982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLPKAVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPMGGMGMGM					
a982	GSGEYGDMIEMGVLPKAVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPMGGMGMGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCTTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTTC	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCAGGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCTG	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TGCGCGCGCC	CTTCGGCTTT	GACAAACAGG	TGACCCCGCG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGcgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTGCG	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTCAGGA	AGTATCCTAC	GGTTTGCGAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGCGCTG	CAGGCGGGCG	ACATCGTCTT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	cggagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgctcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
 1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAC GTCCCCCTGC
 1451 TGGTCatgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986.pep

1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVAGMSI
 151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVND EAGF RKAMD KAGKN VPLLVMRRGN TLFIALNLQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986.seq

1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCGACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
 101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
 151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCGGGC
 201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
 251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
 301 GAATTTTTC AACGCCTCGT CCCGAATATG CCCGAAATCC CCAAGAAGA
 351 AGCAGATGAC GCGCGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
 401 ACGGCTACAT CCTGACCAAT ACCACGTCG TTACCGGCAT GGGCAGTATC
 451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
 501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
 551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
 601 GTCGCGCCA TCGGCGCGCC CTTGCGCTTC GACAACAGCG TGACCGCCGG
 651 CATCGTGTC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTC
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
 751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
 801 CAGCGGCGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
 851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
 901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCCG
 951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
 1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCTT CAGCCTCGAC
 1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
 1101 TACGCGGGA AAGAAGTCA GCCTCGCGT ATGGCGCAAA GGCGAAGAAA
 1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
 1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
 1251 GGTCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
 1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
 1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
 1401 AGCCGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAC GTCCCCCTGC
 1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986.pep..

1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVAGMSI
 151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVND EAGF RKAMD KAGKN VPLLIMRRGN TLFIALNLQ*

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	: :					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
	: : : : : :					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	: : : : : :					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	: : : : : :					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	: : : : : :					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQTHTDSSGKHLVVVRVSDAAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTGT GCAGCACTGT GTGCCGCTTC
51  GCTGGCAGGC TCGGACAAAG CCGGCAGCTT TTTCCGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACGT GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTCA AACGCCTCGT CCCGAACATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGTATAT TCTGACCAAT ACGCAGCTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGCGGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCTTAC GGTTCGCGAC AATCGTTCGG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGAAC ACGCTGTTTA TCGCATTAA CCTGCAATAA

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This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIQEEADD GGLNFGSGFI ISKDGYILT NTHVVTMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ

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1393

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQHTD SSGHLLVVVR VSDAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVAVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPVAVVNIQAAPAPRTQNGSSNAETSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGDNSVTAGIVSAKGRSLPNESYTPFIQTDA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGDNSVTAGXVSAKGRSLPNESYTPFIQTDA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQHTDSSGGHLLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
a986	AGITLQHTDSSGGHLLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq
 1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG

1394

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51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCCCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCCACGA
201 AGCCTTTGCC GCCGCGCGCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTt
351 ggacgacaAC AACAcgcgcg gcttggacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtcgt CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGACGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCTT GATCAGCGAC AGCCTGCAA AAGGACTCGA CCGCGACCG
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCCA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAAATCG GTGACGAGCG GCATAGACGT TACCGTCTCG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCTGTCATGC CAAAACCTTC ATGTGTGAcg gCAAACGCAT
1251 CTTATCGGC TCATTCAACC TCACCCCCG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAA TCGCAGAAAC GATGGAGCGC
1351 AccctCGCGG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

g987.pep

```

1  MKTRSLISLL CLLCSCSSW LPPLERTES RHNTSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAERG VRVRLLLDDN NTRGLDDLLL ALDSDPNIV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPY QKIQTGRIDW QSVQTRLISD SPKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKLGTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAAILLS
501 LLPIEGLL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

m987.seq

```

1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGATATCTAT CTGTGTAACG ACCCCCACGA
201 AGCCTTTGCC GCCGCGCGCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGACGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCT CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCTT CATCAGCGAC GACCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCTT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTCATCGGT TCGTTCAACC TCGACCCCG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGCG ACATCCCGC CACCCGAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1 MKTRSLISLL CLLLCSSSW LPPEERTES RHFTSKPVR LDNILQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VVRLLLDN NTRGLDDLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALRY RETVEQSPY QKIQTGCIDW QSVTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDLAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAANKLS
501 LPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSSSWLPPEERTESRHFTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSSSWLPPEERTESRHFTSKPVLLDNLQIRHTPHNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNVLVYLAERGVRVRLLDN					
	:					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAERGVRVRLLDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLALDSHPNIEVRLFNPFVLRKWRALGYLDFPRLNRRMHNKSFTADNRATI					
g987	NTRGLDDLLALDSHPNIXVRLFNPFVLRKWRALGYLDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFRYWASHAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFRYWASHAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALRYRETVEQSPYQKIQTGCIDWQSVTRLISDDPAKGLDRDR					
g987	KGLQALGYNDETSRHALRYRETVEQSPYQKIQTGRIDWQSVQTRLISDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDLAKLVQDGIDVTVLNSLQATDVA					

1396

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|||||
g987      RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
          |||||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRLQWHD PATRK
          |||||
g987      SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHD PATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA AAKILSLLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA AAKILSLLPIEGLLX
          490      500

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1   ATGAAAACAC GCAGCCTAAT TTCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAGAAGCG GACGGAAAGC CGTCATTTC A
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCGGCCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCGCGCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTTCGC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAAACCA TGCCGTCCTT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACTG
1301 AAATGGGCGT TGTTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCC TAGAAAGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1   MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNSTKPV R LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VVRLLDDDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTFD PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDNRNR LQWHDPATRK TYPNEPEAKL WKRIAAILKLS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLLALDHPNIEVRLNPFVLRKWRALGYLTDPRNLRMHNKSFTADNRATI					
a987	NTRGLDDLLLALDHPNIEVRLNPFVLRKWRALGYLTDPRNLRMHNKSFTADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRRLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRRLISDDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNTSLQATDVA					
a987	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNTSLQATDVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m987.pep	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDNRNRLQWHDPATRK					
a987	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDNRNRLQWHDPATRK					
	430	440	450	460	470	480
	490	500	509			
m987.pep	TYPNEPEAKLWKRIAAILKLSLLPIEGLLX					
a987	TYPNEPEAKLWKRIAAILKLSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq
 1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgagggcg
251 CagtTTGCGc gGCgacaag ctgGATTtGG TCAAATGccg Cgtcgagggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCGTT TTATACGAAC GCCAgatgcg tggTgtcatG CAcggcgaca
401 ccgttACCGT CCGTCCTGCG ggtatggaCC GCAGGGGccg ccgcGAAggg
451 acgtttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTtTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTtGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATtGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTTT GGGCGATTAT GCCGACAGCG
701 GGATGAAAt cgAAATtGCC GTGCGCAAGC ATCATTtGCC GCaccgaTTC
751 AGTGAagcgt gtGcCAAAATC CGcgaAAAA ATtccccgacc ATGTACGCAA
801 AAGCGATTtG AAAGGCCGCG TCGATTtGTG CGACCTtCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTtCGACG ACGCGGTtGT TGCCGAAAAA
901 GTCGGACGCA ATTACCGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCGCCCTT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGTCAA TCCCGATGTC GAGCGTTtGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTtTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAAA TCGACACGCT
1251 TTACAAGCTG TTTAAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTtGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAAA TTGTCCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGCGCA ATGTTtGCGC GGCGGATTTT CTGTTGAAAA
1451 ACAACATAC GGCTtTGTTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGCGCG
1551 CGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGCGCG TTTACGAACC GCATTGCGAA GGGCATtTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACtTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTCGGTGAA ATATTtGAAG GcaaaatCtc ccgggggtgtg
1951 gcaaaTtttg gaATATTtGT CACTtTGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTtGCCG TCCGGGTGCG GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGAG AAAGCGGCAG GCGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGCGGCGG GGAAAGGGAA ATCGAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GGAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KQRYEHLPLS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGEFVP LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGRICSLNPV ERLCMVCDMV VTYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLTKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQQLG LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TYMRDKVGE IFEGKISRGV
651 ANFGIFVTLT DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPAV AESGKKAKKP VPIKVKRKRG KS*

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1399

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51  CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TCGCAAAAAA ATTCCTGTC ATGTACGCAA
351 AAGCGATTTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATTT GCTCGCTCAA TCCCAGTGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCGCGCTGA CCTACAACCA AGTTTGGA
751 TGGATTTGAG ACGGCATCGA CCATCCGTAC AAAGCCCAA TCGACACCT
801 TTACAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCGCT TGTCCGCAAC GATGCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTC CTGTTGAAAA
1001 ACAAGCATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCGTA
1251 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTGCGCGAA GTATTGGAAG GTAAAATCTC CGGCATGACC
1501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATG ACGGCTTGGT
1551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1601 TGGCAATCGA AGCGAACGC AGCGGCATCC GTTCAACAT GGGGACAGG
1651 GTTGCCGTCC GGGTCGCCCC TGCCGATTG GATGACGGAA AAATCGATT
1701 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGC
```

1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)
 1 ..TVLDIVERAQ SKVVGRFYMD RGVAILPEPD KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADGMEIEIA VRKHHLP HQF
 101 SEACAKAAK IPVHVRKSDL KGRVDLRDL LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGDIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKYAALV EQFKGRPDAE LLQVMMLRSM
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
 451 KKSQWALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
 501 SFGIFVTLTG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRENMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKPTA
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGDVTVTRPAGMDRRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED					
	130	140	150	160	170	180
m988.pep	40	50	60	70	80	90
	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA					
g988	KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA					
	190	200	210	220	230	240
m988.pep	100	110	120	130	140	150
	VRKHHLP HQFSEACAKAAKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK					
g988	VRKHHLP HRFSEACAKSAKKIPDHVRKSDLKGRVDLCDLPLVTIDGETARDFDDAVFAEK					
	250	260	270	280	290	300
m988.pep	160	170	180	190	200	210
	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFRRVIPMLPENLSNGICSLNPDV					
g988	VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFRRMIPMLPENLSNGICSLNPDV					
	310	320	330	340	350	360
m988.pep	220	230	240	250	260	270
	ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGDIDHPYKAQIDTLYKL					
g988	ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSDGIGNPHKAQIDTLYKL					
	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
g988	FKILQKKRLARGAVEFESVETQMFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
g988	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPDAE					

1401

	490	500	510	520	530	540
	400	410	420	430	440	450
m988 . pep	LLQVMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
g988	LLQVMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNKRTYTP					
	550	560	570	580	590	600
	460	470	480	490	500	509
m988 . pep	KKSQWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKIS-GMTSFGIFVTLD					
g988	NKSQWQALGVHTSFCERRADDAGRVDENWLKTYMRDKVGEIFEGKISRGVANFGIFVTLD					
	610	620	630	640	650	660
	510	520	530	540	550	569
m988 . pep	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
	570	580	590	600	610	629
m988 . pep	IAGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKKTARGGKVRGRGASAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKGSKTTAEKKKTARCGKVRGRGVPVAESGKKAKKP					
	730	740	750	760	770	780
	630	640				
m988 . pep	VPIKVKRRKGKXS					
g988	VPIKVKRRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988 . seq
1  ATGAATAAAA ATATTAAATC TTAAATTTA CGGGA AAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTGCCCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GGCGGACAAA TTGGATTGG TCAAATGCCG TGCAAGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACCG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGGCG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGA GCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCGGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTGCCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTGCGCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCCGCGCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTTT AAAACCCAAA TCGACACGCT
1251 TTACAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATTGTTT CGCAACCATT TGGGGCCAC GCCCGAAAAA
1501 CTCGCCGCTT TCGCGAGCA GTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1402

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1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCCTA
1701 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1901 TGCGCGATAA GGTGCGCGAA GTATTGCAAG GTAAAATCTC CGGCATGACC
1951 AGTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTCAACAT GGGGACAGG
2101 GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGGAA AAATCGATTT
2151 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
2201 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC
2251 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
2301 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
2351 TAAAAAACG GAAAGGCAAA TCATAA

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This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

a988.pep

```

1 MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVPSKIEAL
51 VRELSIKEEE YEFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVKA
101 HKDRFGFAVP LTPAKDGFV LYERQMRGIM HGDIIVTRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGFRFXMD RGVAILPEP KRLNQSIVLE PDGVARFKPE
201 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF
251 SEACAKAAKK IPDHVRKSDL KGRVDLRDL LVTIDGETAR DFDDAVFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFRR VIPMLPENLS
351 NGICSLNPHV ERLCVVCDMV ITYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPD AE LLQVMLRSM
551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
601 KKSQWALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
651 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
701 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKPTA
751 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

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m988/a988 97.0% identity in 641 aa overlap

```

m988.pep
10 20 30
TVLDIVERAQSKVVGFRFYMDRGVAILEPED
|||||
a988
130 140 150 160 170 180
LYERQMRGIMHGDIIVTRPAGMDGRGRREGTVLDIVERAQSKVVGFRFXMDRGVAILEPED

40 50 60 70 80 90
KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
|||||
a988
190 200 210 220 230 240
KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA

100 110 120 130 140 150
VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK
|||||
a988
250 260 270 280 290 300
VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK

160 170 180 190 200 210
VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFRRVIPMLPENLSNGICSLNPDV
:|||||
a988
310 320 330 340 350 360
IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFRRVIPMLPENLSNGICSLNPHV

220 230 240 250 260 270
ERLCMVCDMVITYAGNIKEYRFYPVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL
|||||
a988
ERLCVVCDMVITYAGNIKEYRFYPVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLYKL

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1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGFTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGFTPEKLAALREQLGLLGLQLGGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
a988	LLQVMMLRSMQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSQWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLTG					
a988	KKSQWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLTG					
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKAKKPV					
	730	740	750	760	770	780
m988.pep	640					
	PIKVKKRKGSX					
a988	PIKVKKRKGSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq

1	ATGACCCCTT	TCACACTGAA	AAAAACCGTC	CTGCTGCTCG	GCACTGCCTT
51	TGCCGCGCA	TCTGTCCACG	CATCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCCG	ACGCGTCGAC	CATCTTCTAC
151	AATCCCGCCG	GCCTGACCAA	ACTCGACAGC	AGCCAGATT	CCGTCAACGC
201	CAACATCGTG	CTGCCAGCA	TTCATTATGA	AGCAGATTCC	GCCACCGACT
251	TTACCGGGCT	TCCCGTCCAA	GGTCTAAAA	ACGGCAAAAT	CACCAAAACC
301	ACGGTCGCAC	CCCACATTTA	CGGCGCATAC	AAAGTCAACG	ACAATCTGAC
351	CGTGGGCTTG	GGCGTGTACG	TCCCCTTCGG	CTCTGCCACC	GAATACGAAA
401	AAGATTCCGT	GTTGCGCCAC	AACATCAACA	AACTCGGTCT	GACCAGCATC
451	GCCGTCGAAC	CTGTCGCCGC	GTGGAACATC	AACGAACGCC	ATTCCTTCGG
501	CGCAGGCATC	ATCGCCCAAC	ATAATTCCGC	CGAACTGCGC	AAATATGCCG
551	ACTGAGGAAT	CCCAAAAAAA	GCGCAAATGC	TGCAAGCAAC	ACCTTCTAAT
601	CCTACTGCCG	CTGCTCAAAT	CAAGGCCGAC	GGACACGCCG	ATGTCAAAGG
651	CAGCGATTGG	GGCGTCGGCT	ACCAACTGGC	GTGGATGTGG	GACATCAACG
701	ACCGCGCGCG	CGTGGGCGTG	AACTACCGTT	CCAAAGTTTC	ACACACGCTC
751	AAAGCGGATG	CCGAATGGGC	GGCAGACGGC	GCGGCGGCGA	AACAACAGTG
801	GAATGACAA	ATGCTCACAC	CGCTCGTTTA	CACGGCGAAT	GAAAAAGCCA
851	GTGTCAAAAT	CGTAACGCCT	GAGTCTTTGT	CCGTACACGG	CATGTACAAA

1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAAC TTGGA CGCGCCACAG
951 CCGCTTCAAT AAGCGGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacc
1151 GCATGAACAG CCTGCCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TCGGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

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This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
1 MTPFTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GVVYVFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAIKAD GHADVKGS DW GVG YQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGM YK
301 VSDKADLFGD VTWTRHSR FN KAELFFEKEK NIANGKKS DR TTITPNWR NT
351 YKVGLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSA GM
401 KYHIGKNHV V DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCGG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTTCAT TATGAGGCGG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGTTC GAAAAGCGGC
301 AAAATCACA AAACCAAGGT CGCGCCCGAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTGTC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAGGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAAC TAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAGCC CGCGTTAAAA TC GTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCCGCCA
951 CGTAACTTGG ACGCGCCACA GCGCTTCGA TAAGCGGAA CTGTTTTTGT
1001 AAAAAAGAAA AACCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCAC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCCG
1151 TCCGCAACCG CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCGC CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAAACCAG CCGACATCAT CCGTCTGCAA TACACCTACA AATTCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
1 MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEK SVLRHNINKL
151 GLTSIAVEPV AAWKLND R HS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPN GVA EAAKIQADGH ADVKGS DWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGM YKVS D KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
 401 WFSAGMKYHI GKNHVVDAAI THIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
m989	MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
m989	TKLDSSQISVNNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSKAEILTAKPPKNGVAEAAKIQADGHADVKGSDWGVGYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES				
m989	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMKYVSDKADLFGDVTWTRHSRFNKAELFFEKEKNIANGKKSDRTTITPNWRNTYK				
m989	LSVHGMKYVSDKADLFGDVTWTRHSRFDKAEKVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
m989	VGLGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	400
	420	430	440	450	460
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq

1	ATGACCCCTT	CGGCACTGAA	AAAAACCGTC	CTACTGCTCG	GCACTGCCTT
51	TGCCGCGCA	TCCGCACAAG	CCTCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCGG	CCGCAGAAGC	CGCCGACGCA
151	TCGACCATCT	TCTACAACCC	TGCCGGCCTG	ACCAAACCTG	ACAGCAGCCA
201	GATTTCGCTC	AACGCCAACA	TCGTGCTGCC	CAGCATTTCAT	TATGAGGCGG
251	ATTCGCCAC	CGACTTTACC	GGGCTTCCCG	TCCAAGGTTC	GAAAAGCGGC

1406

```

301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAATC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCGGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GGCAGAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTTC GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCCTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCAGC GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGCGCGT CTTCCGCACG TTTCAAAAAC
1351 CACGCCGACA TCATCGGCTT GCAATACACC TACAAATTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```

a989.pep
1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYK VNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWFGYQ LAWMDINDR ARVGVNYRSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMYKVSDKA DLFGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKFK*

```

m989/a989 93.1% identity in 467 aa overlap

```

          10      20      30      40      50      60
m989.pep  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          |||
a989      MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          10      20      30      40      50      60

          70      80      90     100     110     120
m989.pep  TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          |||
a989      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          70      80      90     100     110     120

          130     140     150     160     170     180
m989.pep  LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT
          |||
a989      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHT
          130     140     150     160     170     180

          190     200     210     220     230     240
m989.pep  SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWFGYQLAWMWDI
          |||
a989      SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWFGYQLAWMWDI
          190     200     210     220     230

          250     260     270     280     290     299
m989.pep  NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
          |||
a989      NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES

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1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGKSDRTTITENWRNTYKV					
a989	LSVHGMKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTI VNGKSDRTTITENWRNTYKV					
	300	310	320	330	340	350
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
	360	370	380	390	400	410
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
	420	430	440	450	460	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CCGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTTAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTAGTA CGCTCAAACA GACGATGCCG GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGGAC AGGTGTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCTT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAACTGAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAAACGGC GGATTCCGGT TCGTTTGGCT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGCGGCG CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
1201 GGCGGCAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGATGGTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCRAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCCGAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGCGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGAATGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCTT TTTGCTTTCG GTAACGGTGT CAATCTTCAG
1651 CCTTTTGGCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTSPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGWRKGVQ IGGEVFRQON EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLOP
501 QAQFTYLGVN GGFTDSEGTA VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGCG ACTTCCCATT
101 ATTTTTCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AACTACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCG GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTC AATCGAAAA
501 CAAATCCACG GTCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGCGG TGGTTTGGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTCCGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGGCGGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GCGGCGAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCGT TGTCCGAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAAGTGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTTAATGT TTGACACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKYITDITY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTSPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGRRKGVQ IGGEVFRQON EGSRLAIGVM

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1409

401 GGRAGQHASV NGKGGAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGA VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWL*F

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m990.pep	SGILAVDNMPVVKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	SGILAVDNMPVVKYITDTYGDNLKDAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m990.pep	KFSTLKQTMPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m990.pep	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGADFLFGYDVRESDKP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m990.pep	ALTFEDKVSGQSGVVLERRPENLKTLDGRKLIAAKTADSGSFQKQNYRQGLYELLKQC					
a990	ALTFEEKVSGQSGVVLERRPENLKTLDGRKLIAAEKADSNSFQKQNYRQGLYELLKQC					
	250	260	270	280	290	300
	310	320	330	340	350	360
m990.pep	EGGFCLGVQRLAIPAEAVLYAQAYAAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQAYAAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m990.pep	RSHQNIRGGAAADGWRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGAGSD					
a990	RSHQNIRGGAAADGRRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGAGSY					
	370	380	390	400	410	420
	430	440	450	460	470	480
m990.pep	LYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
	490	500	510	520	530	540
m990.pep	ALVAEGIVGKGNVRFYLQQAQFTYLGVNNGGFTDSEGTAVGLLGSGQWQSRAGIRAKTR					
a990	ALVAEGVVGKGNVRFYLQQAQFTYLGVNNGGFTDSEGTAVGLLGSGQWQSRAGIRAKTR					
	490	500	510	520	530	540
	550	560	570	580	590	600
m990.pep	FALRNGVNLQPFPAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQPFPAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990 . pep	YGKRTDGDKEAALSLKWLF	X				
a990	YGKRTDGDKEAALSLKWLF	X				
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992 . seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACGTGAG  GGGACGTGGG  TTTCGACGCG  CCCGTCGCCC  GACGGGCATC
201 GGGGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCCT  TCACGTCATC  GACGGCGACG  GCGCGAAACA  TAAAATTCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GTACACGTTT
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  AGTGTACGTG
401 TGTTTGAAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCGCGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAGAAGC  AGCAGGATAA  GCGCGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAAATCCG  AAGCGCCGTG  GCGGTACCGC  CGGCGAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992 . pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAFEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDVGEWL  GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992 . seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GTTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGGCGGGCAG  GGGACGGCGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GGGGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTGCAGC
401 TGTTTCGATC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAGAAGC  AGCAGGATAA  GCGCGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAAATCCG  AAGCGCCGTG  GCGGTACCGC  CGAGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992 . pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAFEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

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	10	20	30	40	50	60
m992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLDVGAAGDAGSDA					
g992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLDVGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVS RVFTDRYQREVAQVSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVS RVFETDRYQREVAQVSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWMDAVGEWLGIX					
g992	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWMDSVGEWLGIX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

a992.seq

1	ATG	TTC	CAG	CAC	GGC	ATC	GGCA	TTT	GAAAA	AAT	ATG	CAG	ATTA	AAAAA	AAT	CAT
51	GAA	ATG	GCT	T	CCC	GTC	GCCT	TGT	CGCT	TTT	GGT	GCG	TTG	GGT	TAT	ACGG
101	GGT	ACG	GCAG		CGA	GCG	GGTG	CGG	ACG	CGCG	TTG	CCG	TACT	CGA	CGT	ACTC
151	GGC	GCG	GCAG		GGG	ACG	CGGG	TTT	CCG	ACG	CGC	CCC	CCCC	GCC	GAG	CATC
201	GGC	GAA	ATCC		GGC	CAC	CGCT	AC	CAG	GCAC	GGT	GTCC	AAA	GTCT	ATG	CAGC
251	GCG	CAC	CCCT		TC	ACG	TTATC	G	ACG	GCG	CAC	GCG	GAA	CA	AAAT	CCGG
301	ATG	GCG	TATA		TC	GAC	CGGCC	G	GAG	ATG	AAA	CAG	GCT	TAC	G	CACG
351	GCG	CACA	CAAC		CT	GCG	CGCG	G	CGG	CGA	AGG	CAG	GAA	AGT	C	AGCG
401	TGT	TCA	CAC		CG	ACC	GCCTAC	C	CAG	CGC	GAAG	TGC	GCG	AGG	T	CTGT
451	AAA	ACC	GATT		TG	AAC	CTGAT	G	CAG	GTG	CAG	GAC	GGG	CGG	C	GTGC
501	TAA	AGT	TAT		GCT	AA	AGAAC	A	AGC	AG	GATAA	GGC	GAT	TTT	G	CCGAT
551	CCG	ACG	CTCA		AAT	TCA	GGCG	G	GAA	AGG	GAAC	GCA	AAG	GAT	G	TGGA
601	AAA	AAT	CCGC		AAG	CGC	CGTG	G	GGC	GTACC	CGC	CGG	CAG	GCA	G	AGCG
651	GGG	CA	ATAAG		GAT	TG	GATGG	A	ATG	CCG	TGGG	CGA	ATG	GTG	G	GCATT
701	AA															

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

a992.pep

1	MFR	RHR	HLKN	MQIK	KIM	KWL	PVAL	SLL	GAL	GYT	GYG	SEAV	RTAV	AVLD	VLD
51	GA	AGD	AGSDA	PARR	RASAKS	GHRY	TGT	VSK	VYD	GDT	HLVI	DGD	GAK	HKIR	
101	MAY	IDAP	EMK	QAYG	TRSRDN	LRAA	EGRK	V	SVR	VFT	DRY	QRE	VAQ	VSVG	
151	KTD	LNLM	QVQ	DGA	AWHYKSY	AKEQ	QDKADF	ADY	ADA	QIQ	A	ERER	KGL	WKA	
201	KNP	QAP	WAYR	RAG	RS	GGGNK	DWMD	AVGE	WL	GIW*					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLDVGAAGDAGSDA					
m992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLDVGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

a992.pep  LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
          |||
m992      LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
          |||
          130      140      150      160      170      180

          190      200      210      220      230
a992.pep  ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGKNKDWMDAVGEWLGIWX
          |||
m992      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGKNKDWMDAVGEWLGIWX
          |||
          190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1  CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATCCG ATGGTGGAAA
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCGCTCTGC TTGCCTACGA GCAAATGAAA
301 CTGGCGGCGC AGGGTTTGGG CGCGCTGCCG CGTGGCGGAC GGGATTTTCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCAGAG
401 TTTACATCGC CGATTGATG CAGGCATGGT TGGGCATCTT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCAGCG
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCGGC ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1  LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVEITGOYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVD EADPRAELV RLLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1  TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATCCG ATGGTGAAGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCGCCTGC TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGGG CGCGCTGCCG CGAGCCGGAC GGGATTTTCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAAA GAAACCATCT CCGTGCAGCG
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCGGC ACACGAGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1  LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVKITEOYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RLLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIET	YQFDLAAEYLLMA			
g993	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVEITGQYLHYIAQMEAY	QFDLAAEYLLMA			
	10	20	30	40	50	60
m993.pep	70	80	90	100	110	120
m993.pep	AMLEIKSRLLLPRTETVEDEEADP	RAELVRRLLAYEQMKLAAQGLDAL	PRAGRDFAWAY			
g993	AMLEIKSRLLLPRTETVEDEEADP	RAELVRRLLAYEQMKLAAQGLDAL	PRAGRDFAWAY			
	70	80	90	100	110	120
m993.pep	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQAWL	GILSRKHTRSHEVIKETISVRAQMT	AILRRLNKGH			
g993	LPLEIAAETKLPEVYIADLMQAWL	GILSRKHTRSHEVIQETLSVRAQMT	AILRRLNKGH			
	130	140	150	160	170	180
m993.pep	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAYVVNFIALLE	LAKEGLVRIVQEDGFGEIRISLN	HEGAHSDGISG			
g993	ICRFHALFNPQGAAYVIVNFIALLE	LAKEGLVIVQEDGFGEIRISLN	HEGAHSDGIFG			
	190	200	210	220	230	240
m993.pep	249					
m993.pep	TRGGRDVFX					
g993	TRGGRDVFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATTCCG	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGGCGG	CGGAATATCT	TTTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCGTGC	CGAGTTGGTG	CGCCGCCTGC	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGGTTGGA	TGCGCTTCCT	CGTGGCGGCC	GGGATTTCGC
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGCC	TGAGTATTTT	GTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCGCGC
501	GCAAAATGACG	GCAATCCTGC	GCCGTTTGAA	CAAACACGGG	ATATGCAGGT
551	TTACGACCTT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTCATCGCAC	TGTTGGAGCT	TGCCAAGAA	GGTTTGGTCG	GAATCGTACA
651	GGAAGTCGGT	TTCCGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTCAGACGG	CATTTCGGC	ACACGGGGCG	GGCGCGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSFGQ	PLDLLYLIR	KQNI	DVLDIP	MVKITEQYLH	YIAQIET	YQF
51	DLAAEYLLMA	AMLEIKSR	LLPRTET	VED	EEADPRAELV	RRLLAYEQM	K
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLSILSRA		
151	KHTRSHEVIK	ETISVRAQMT	AILRRLNKGH	ICRFHDLFNP	EQGAAYVVVN		
201	FIALLELAKE	GLVGIVQEVG	FGEIRISLNH	EGAHSDGISG	TRGGRDVFX		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIET	YQFDLAAEYLLMA			
m993	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIET	YQFDLAAEYLLMA			

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
	AMLEIEKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
m993						
	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLSILSRKHTRSHEVIKETISVRAQMTAILRRLNKHG					
m993						
	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLVGIVQEVGFGEIRISLNHEGAHSDGISG					
m993						
	190	200	210	220	230	240
a993.pep	249					
	TRGGRDVFX					
m993						
	TRGGRDVFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGCG TTCTTACCGC
51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCT GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GCGGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAGAAAGT TCCCAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AAAAGGAAAA CATTCGCCGC GTCTCGTCG
401 GCGTGCCGCA CATCACACTG GCGCGTTGT TCGGGCATTG GAGCGACCAT
451 CCGCTGTATG AGGATTGTG CAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGTGCGGC GAAATTTTGG GCAATAATA TCTGAAATCC GACCAATATC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTCG CCGAAATTTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1 MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPAQLQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPEE QTRANIAKII ETQKENIPA VLVGVPHITL GALTGHLSHDH
151 PLYEDLSEY GIPLFGGAWA EILGNLNLKS DQIHANGKGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGCG TGCTTACCGC
51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCT GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCTT
151 GCGGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAGAAAGT TCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCCGCC GTCTCGTCG
401 GCGTGCCGCA CATCACACTG GGTGCGTTGT TCGGGCATTG GAGCGATCAT
451 CCGCTGTATG AGGATTGTG CAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CCGTGCGGC GAAATTTTGG GCGATAATA TCTGAAATCC GACCAATATC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTTG CCGAAGATTG GAATCAATTT
601 TTGAGAAAAC AGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1 MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPAQLQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG

```

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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEY GIPFLGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

	10	20	30	40	50	60
m996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPQLQK					
g996	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPQLQK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m996.pep	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
	70	80	90	100	110	120
	130	140	150	160	170	180
m996.pep	ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNNLKS					
g996	ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGNNNLKS					
	130	140	150	160	170	180
	190	200				
m996.pep	DQIHANGKGYRKFAEDLNQFLRKQGR					
g996	DQIHANGKGYRKFAENLNQFLRKHGFRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq
 1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TCCTTACCGC
 51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAATTCCTC GAAGGAAGCA
 101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCC
 151 GCGGAATCCT ACCCCGCGCA ACTGCAAAA CTGACGGGT GGAATATTGT
 201 CAACGGCGGC GTATCGGGCG ATACATCCGC CCAAGCCCTG TCGCGCCTGC
 251 CCGCGCTGTT GGCACGCAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
 301 AACGACTTTC TCGCAAAGT TCCCAAGGAG CAGACCCGCG CCAATATCGC
 351 GAAATCATC GAAACCGTGC AGAAGGAAA CATCCCGGCC GTCCCTCGTCG
 401 GCGTGCCGCA CATTACCTTG GCGCGTTGT TCGGGCATT GAGCGATCAT
 451 CCGCTGTATG AGGATTGTG CGAGGAATAC GGCATTCCGC TGTTCGGCGG
 501 CCGTGCGGCG GAAATTTTG GCGATAATA TCTGAAATCC GACCAAATCC
 551 ACGCCAACGG CAAAGCTAT CGGAAATTG CCGAAGATT GAATCAATT
 601 TTGAGAAAC AGGGGTTTAG ATAA

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep
 1 MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
 51 GESYPQLQK LTGWNIVNGG VSGDTSQAQ LRLPALLARK PKLVIVGIGG
 101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEY GIPFLGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

	10	20	30	40	50	60
a996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPQLQK					

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```

|||||
m996  MNRRFTLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK
      10      20      30      40      50      60
      70      80      90      100     110     120
a996.ppep  LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
|||||
m996  LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
      70      80      90      100     110     120
      130     140     150     160     170     180
a996.ppep  ETVQKENIPAVLVGVPHITLGALFGHLSHDHPLYEDLSEEGYIPLFGGAWAEILGDNNLKS
|||||
m996  ETVQKENIPAVLVGVPHITLGALFGHLSHDHPLYEDLSEEGYIPLFGGAWAEILGDNNLKS
      130     140     150     160     170     180
      190     200
a996.ppep  DQIHANGKGYRKFAEDLNQFLRKQGFR
|||||
m996  DQIHANGKGYRKFAEDLNQFLRKQGFR
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTC TCGGCGCAGG
51  CTGGGCGGCG TTGTCCGCGG CCGTCACCTT GCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGCGCGG CAGGCGGGCG GAAGGCGCGG CACACTGGCC
151 GGAATATACG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TCGCCTGTAT GAAAACCATC GGTTCAGACC
251 CCCGTGCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTGCCCCTGC CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAATGCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTAAT
501 GCAGTTTGG CAGCCCTTGG TCTGGGCGCG GCTCAACACG CCTTTGAAA
551 CCACAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCCGCCCTGG CCGAGCTTCA ACGGCTCGG CGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCTCCCGGA CGGAAAAGTC
751 CTCGTCACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCGCGC GCGCTCCTGC CCGAAGGCAC GCCGGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGCGC CGCCCGCTG ACCGGCATg CCGAcggcAC
951 ggcaCaatg CTGCTTTgcc cgGGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAAttagc GTTTCGAcc GCGtcggcgc Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.ppep (partial)
1  MNNTPHRPRK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVRLMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKORN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKSQSYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLEPGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTC TCGGCGCAGG
51  CTGGGCGAGG CTGTCCGCGG CCGTCACCTT GCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGCGCGG CAGGCGGGCG GCAGGCGCGG CACACTGGCC
151 GGAATATACG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TCGCCTGTAT GAAAACCATC GGTTCGATC
251 CCCGTGCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTGCCCCTGC CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAATGCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTGAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGAAA

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1417

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551 CCGCAAGCCT GCGCGTGTG TGCAACGTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCTTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCGTATGC CGTCTGAACA CCTCCCGGA CGGGAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCCGC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCCTGCC CGCCCGCTG ACCGCGCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCGCT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCCG GACTTGTCTG GGTTCACCG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCCGGAC TACCCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```

m997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLAGY RGVRLMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKSQSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVW LLCRGRGLP ENEVSAVISV SDRVGAFANR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAQDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

g997.pep	10	20	30	40	50	60
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
g997.pep	70	80	90	100	110	120
m997	NGQHILLAGYRGVRLMKTIIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
g997.pep	130	140	150	160	170	180
m997	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
g997.pep	190	200	210	220	230	240
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
	190	200	210	220	230	240
g997.pep	250	260	270	280	290	300
m997	RLNTLPDGKVLVNGEAFDAAILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
	250	260	270	280	290	300
g997.pep	310	320	330	340	350	
m997	AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFANR					
	310	320	330	340	350	

1418

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGCGC TTGTCCGCGC CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGCGCGC CGCACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGCGGTGT TCGCCCTGAT GAAAACCATC GGTTAGACCC
251 CCCATGCCGC CTTTTTGC GC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTGCCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCGCGGCGCG TACCGTCCGC ATTCAAAGCC AACTGCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTAAT
501 CGAGTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCGGCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCATATGC CGTCTGAAAC CCCTCCCGGA CGGGAAGTG
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
801 CCGCGCCGCG GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 CGCGAACCAG TCCGCTTGCC TGCCCCGCTG ACCGGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGGCGAACC CGAAGCGTGC GCGTCATCAC CGAAAACGC GCCACAACCG
1151 CAGCCGATGC CCGCGCGCGG GATTGTGCTG GGTGACCCG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCCAGAC TACCCGCGCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCCGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVRLRMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNPEPFDAV VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLR
301 AEPVRLPAPL TGLADGTVQW LLCRGRLGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVRLRMKTI GSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVRLRMKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSGVLT KKSQSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLT KKSQSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSGVLT KKSQSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLT KKSQSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC					

1419

```

m997      PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEPFDAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           |||||
m997      RLNTLPDGKVLVNGEAFDAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
           |||||
m997      AEPVRLPAPLTGLADGTQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRHRIFFPAGDYLHPDYPATLEAAVQ
           |||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRHRIFFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTATC
51  AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACTTTTTC CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGAATAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QSKTAQAE PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKDCGY DLTLMDFGA IALKLDEQQK
101 IRAISVGYIL KTDGERGQNL VNNAINGLHS IQAVLSLTIT DKLGESEAGK
151 QLFTALTEVV KESNOTGATA QKDV PADGIL YSVVFEKETN TIAIIGRKQP
      *

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

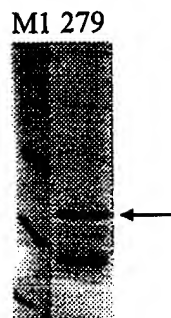
17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

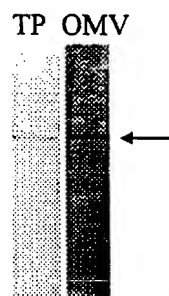
Fig. 2

279 (10.5 kDa)

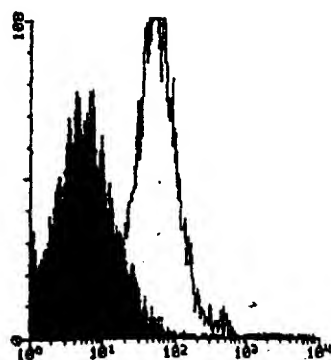
A) PURIFICATION



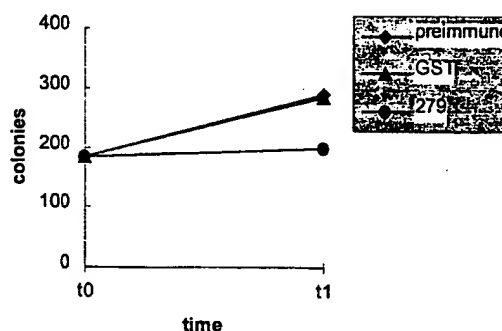
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

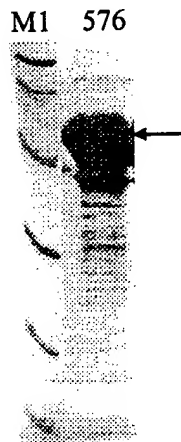
279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 3

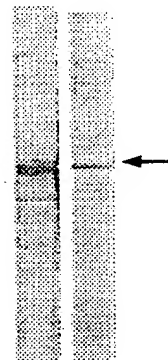
576 (27.8 kDa)

A) PURIFICATION

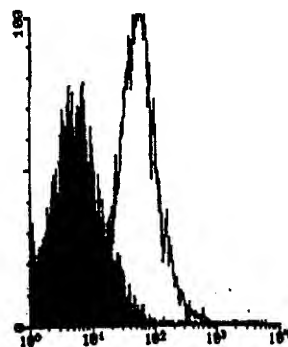


B) WESTERN BLOT

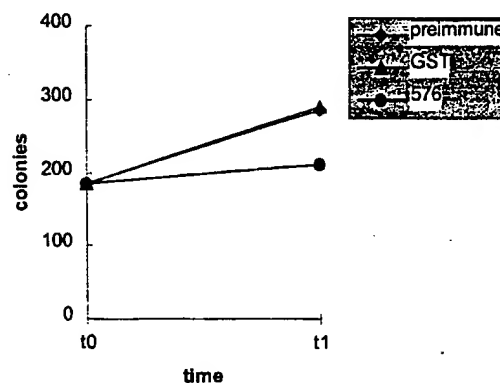
TP OMV



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

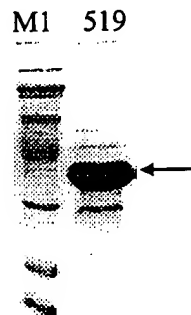
576

The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 4

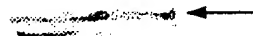
519 (33 kDa)

A) PURIFICATION

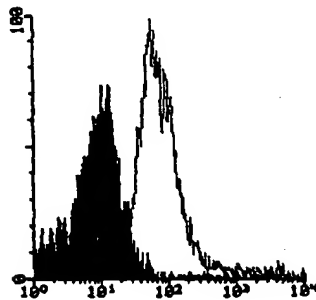


B) WESTERN BLOT

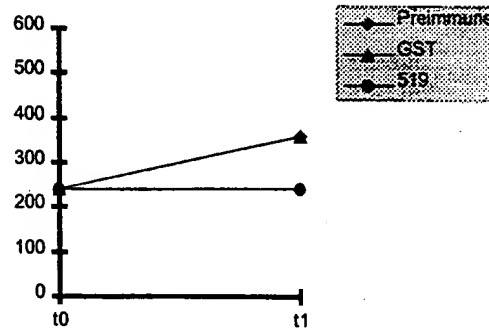
TP OMV



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

519

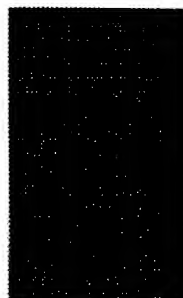
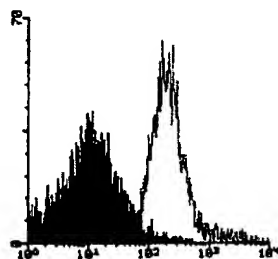
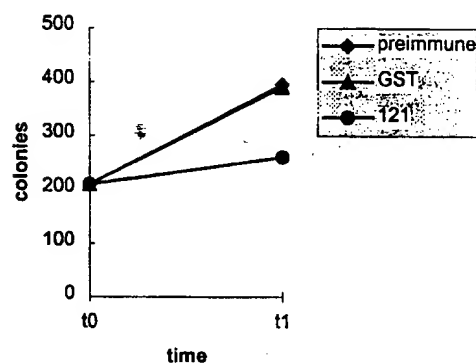
The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION**

M1 121

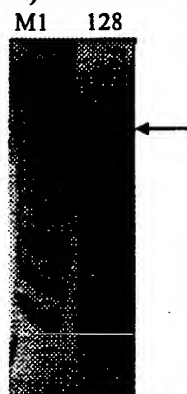
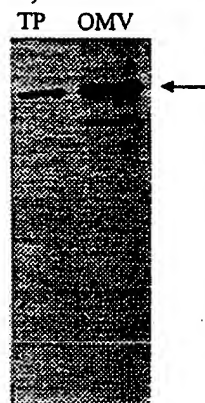
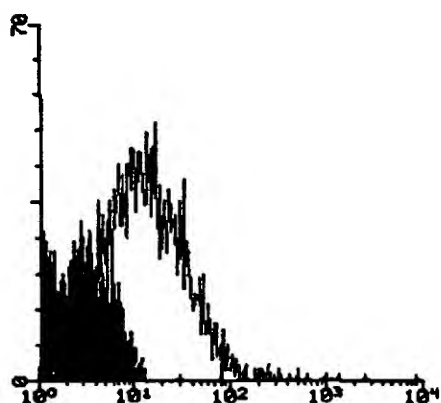
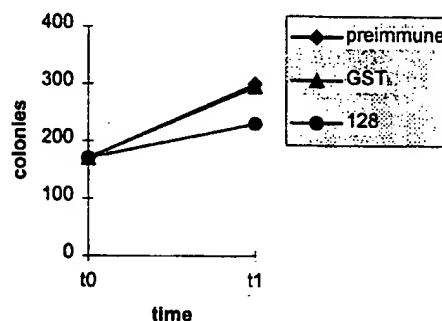
**B) WESTERN BLOT**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

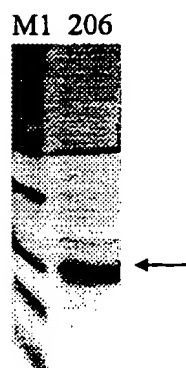
Fig. 5

128 (101 kDa)**Fig. 6****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****128**

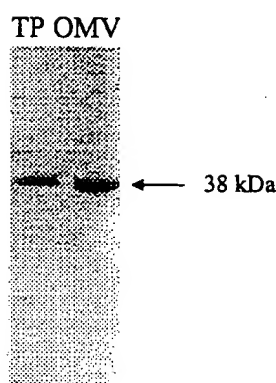
The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

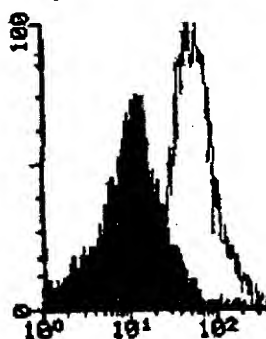
A) PURIFICATION



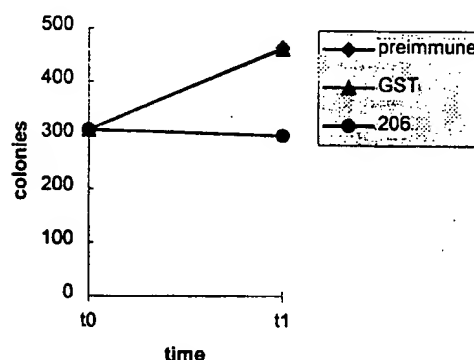
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

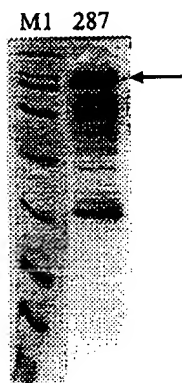
206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C) is shown the FACS analysis, in panel D) the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

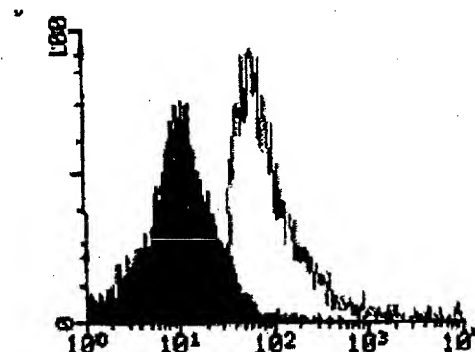
287 (78 kDa)

Fig. 8

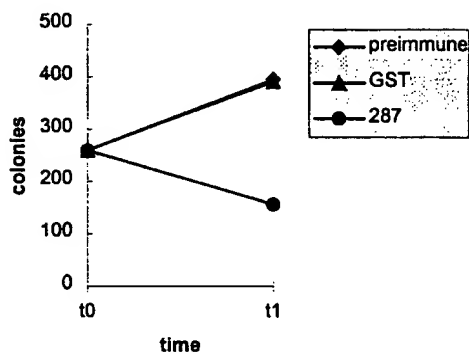
A) PURIFICATION



B) FACS



C) BACTERICIDAL ASSAY

D) ELISA assay : positive

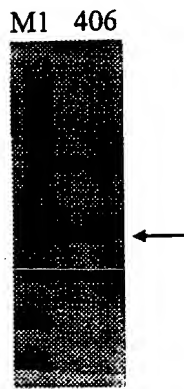
287

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

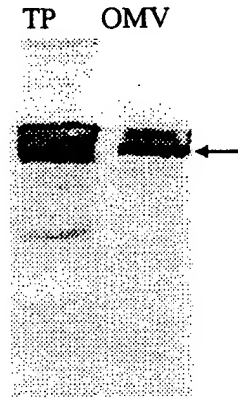
406 (33 kDa)

Fig. 9

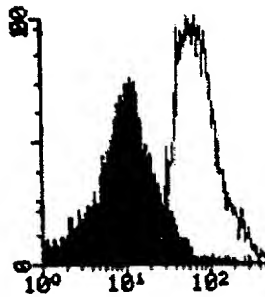
A) PURIFICATION



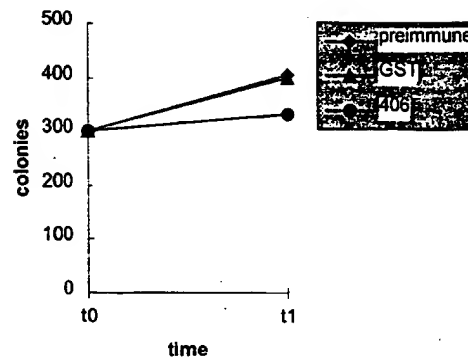
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay : positive

406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

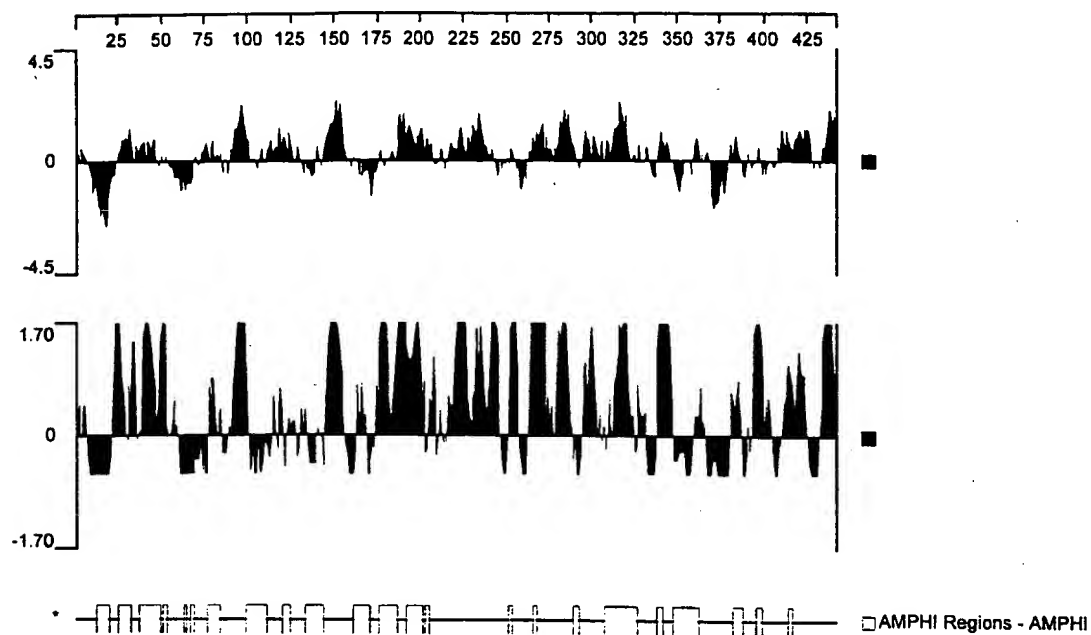
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

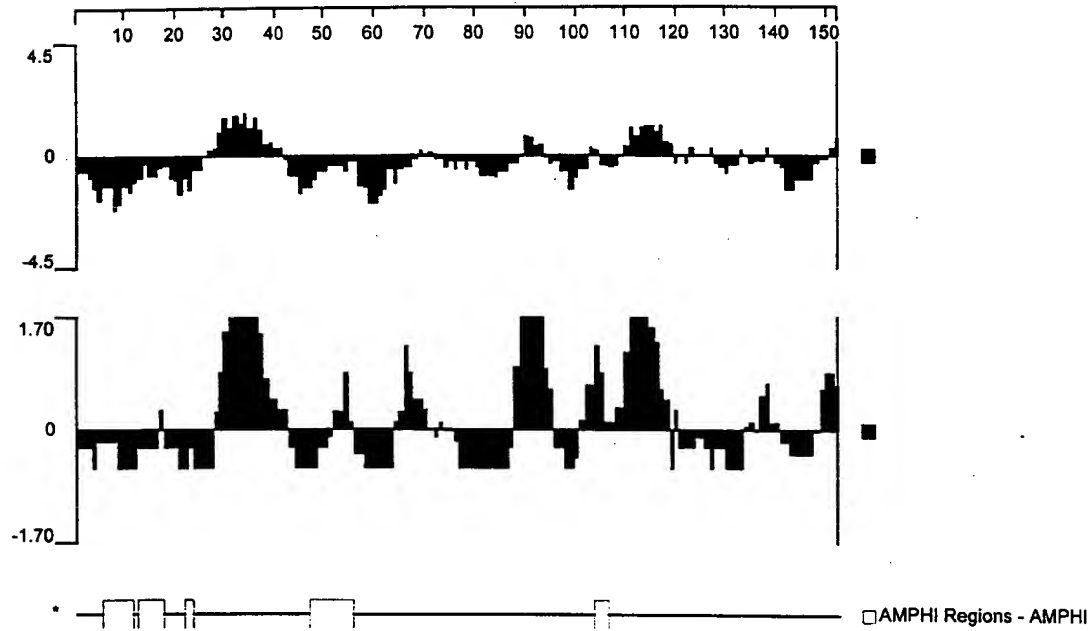
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

11/30

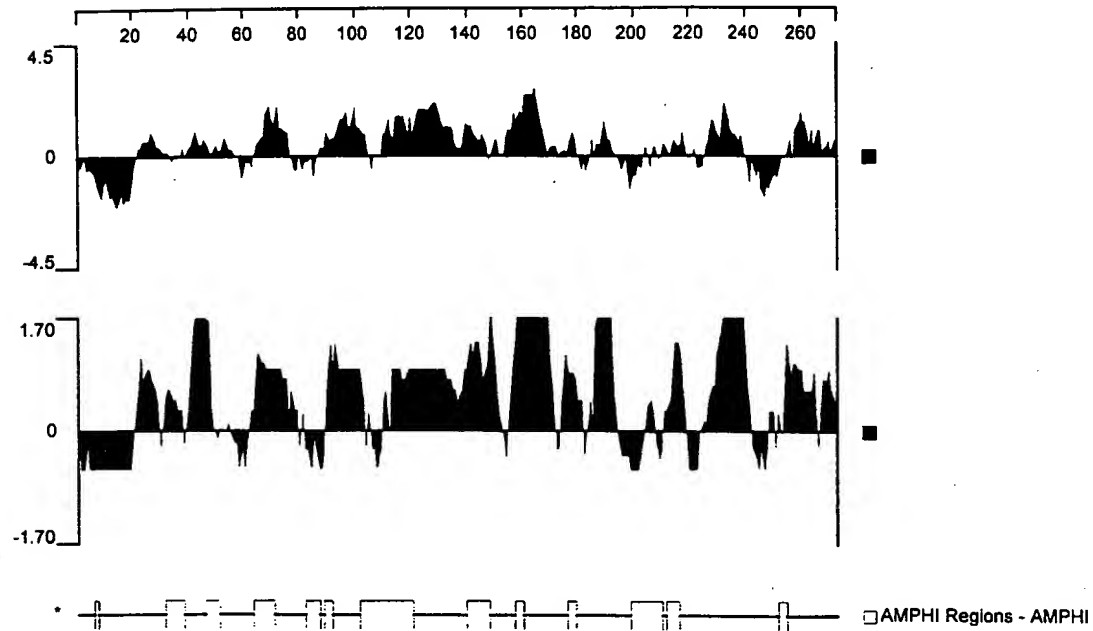
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

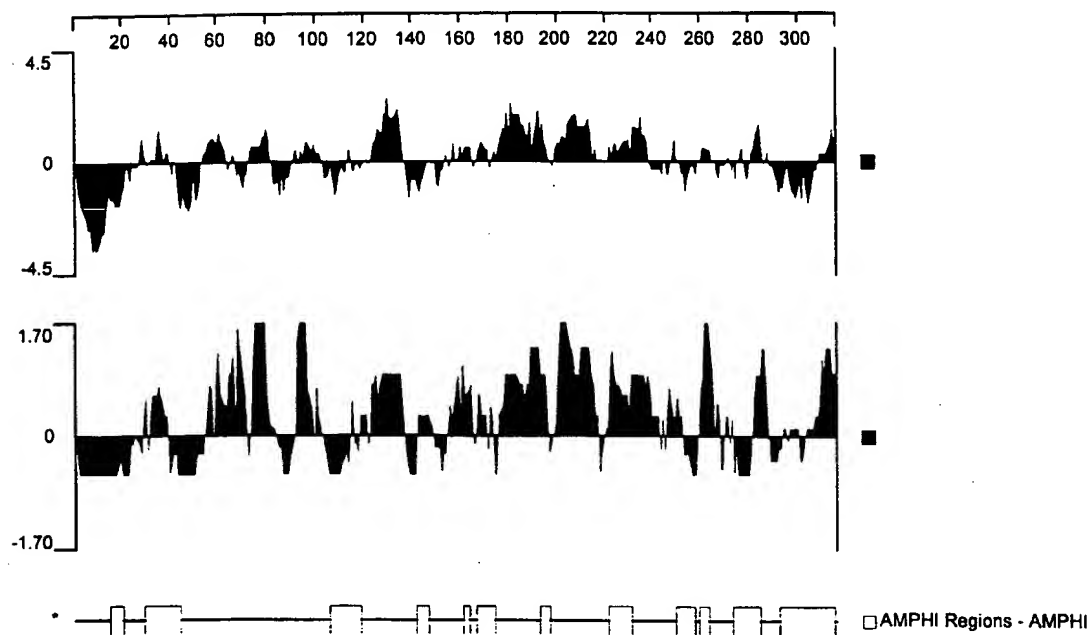
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

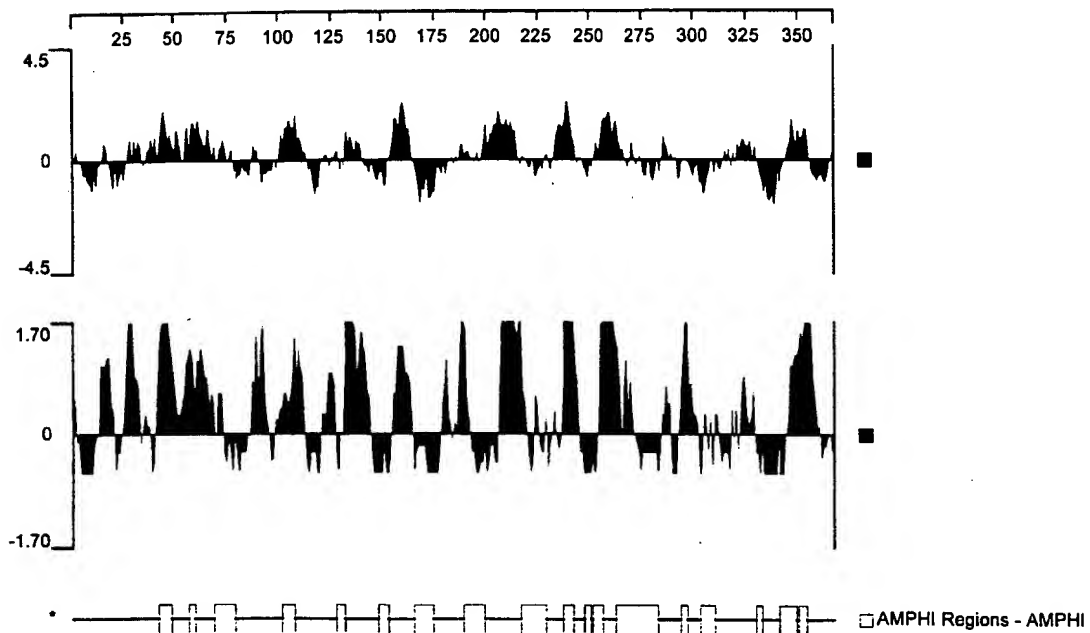
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

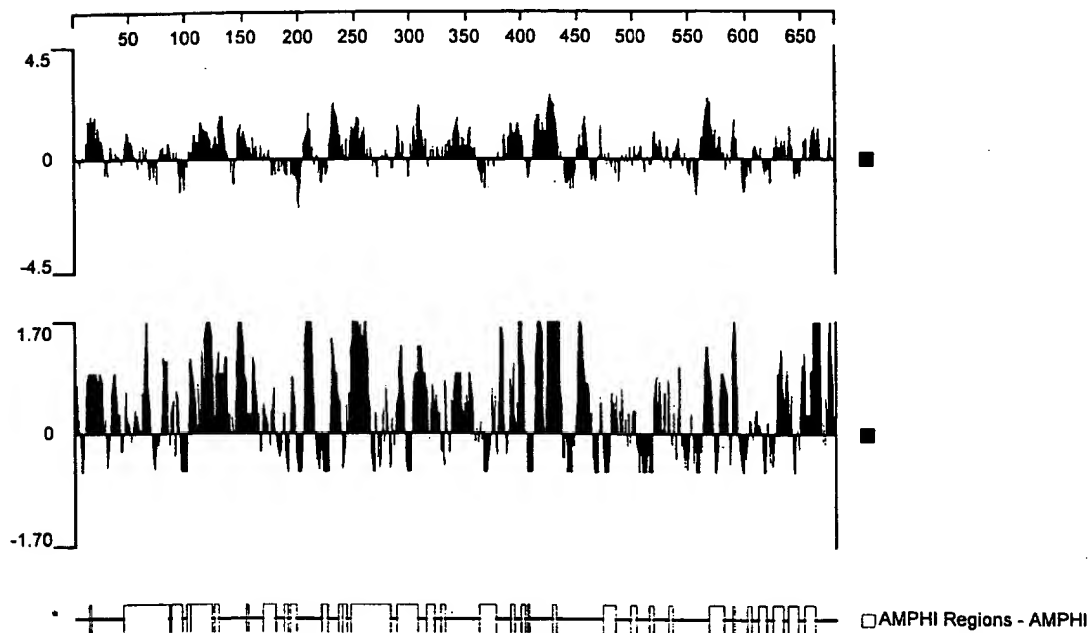
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

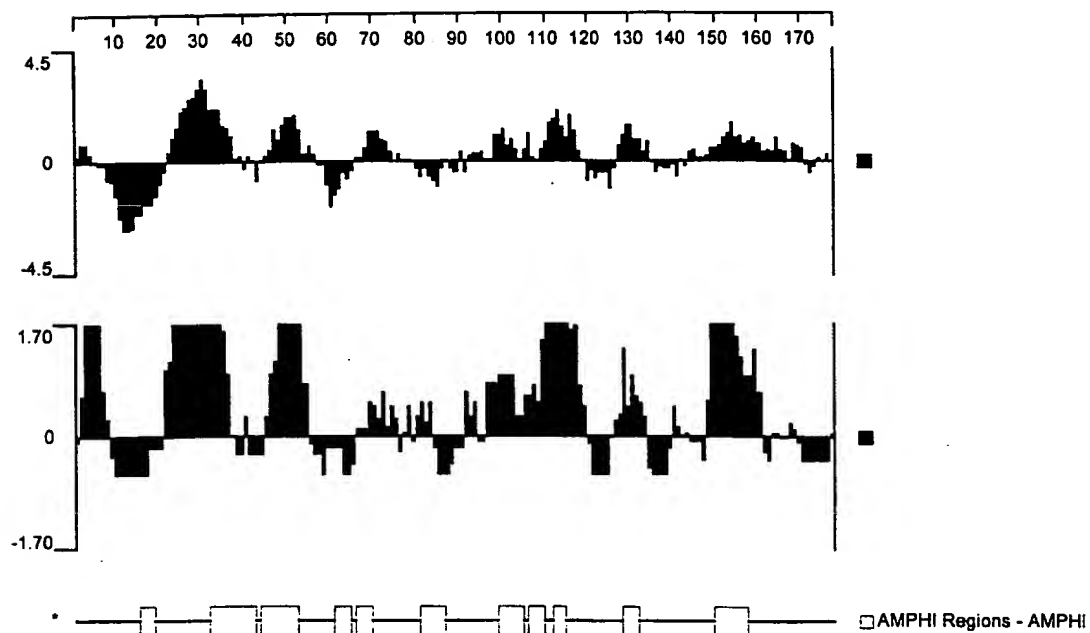
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

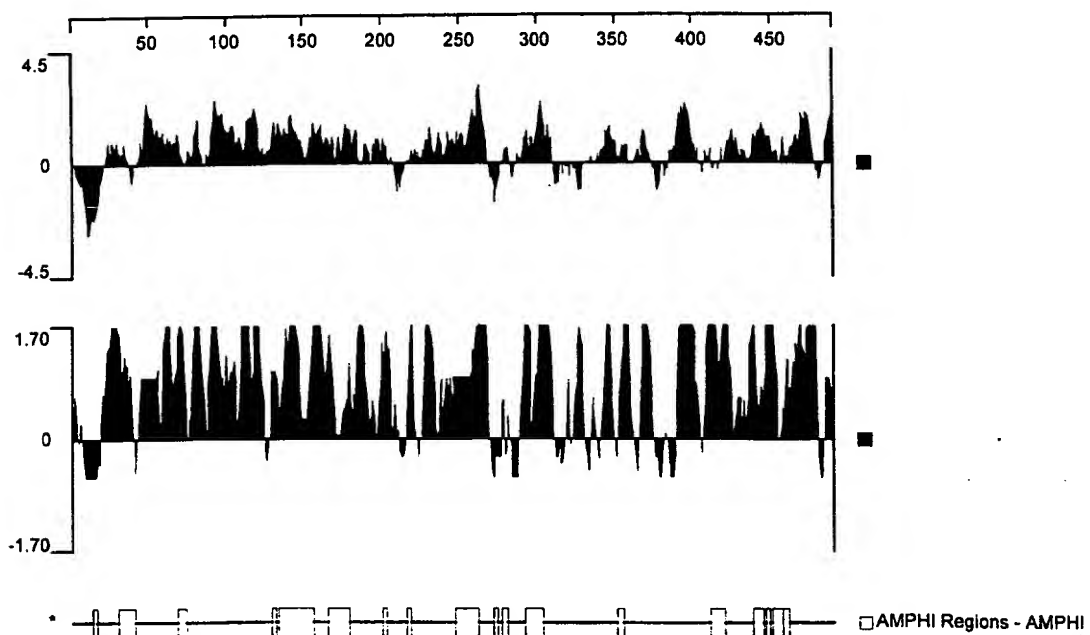
287Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

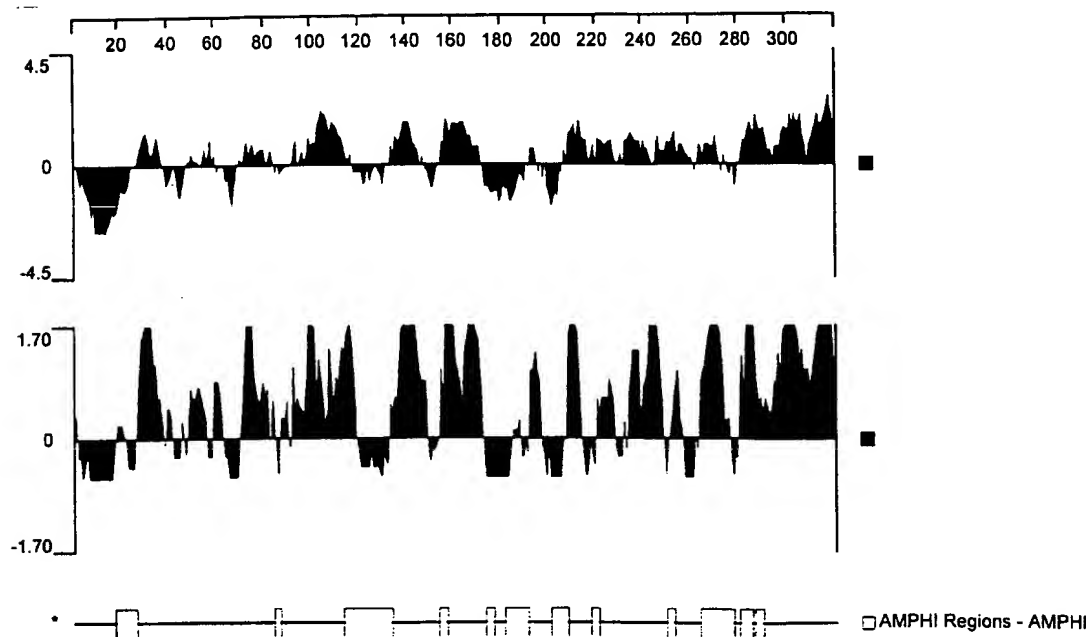
406Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

Fig. 19A

Fig. 19B

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

Fig. 20A

gnmq09	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq31	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
fa1090	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq32	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq33	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq01	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq05	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq08	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq02	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq03	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq04	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq07	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq10	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq11	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq13	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq15	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq16	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq17	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq19	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq21	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq22	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq23	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq24	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq25	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq27	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq28	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq29	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
z2491	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq14	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq18	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT
gnmq26	121	YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGILLGALVSAVVNQIANSLT

gnmq09	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq31	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
fa1090	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq32	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq33	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq01	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq05	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq08	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq02	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq03	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq04	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq07	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq10	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq11	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq13	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq15	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq16	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq17	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq19	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq21	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq22	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq23	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq24	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq25	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq27	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq28	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq29	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
z2491	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq14	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq18	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK
gnmq26	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK

Fig. 20B

```

287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVVE.....KETEAE
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVVE.....KETEAE
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVVE.....KETEAE
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVVE.....KETEAE
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVVEEDVGEEVLPKEKKETEAE
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVVEEDVGEEVLPKEKKETEAE

287_14 50 KEDAPQAGGQGGGAPSNQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
287_2 50 KEDAPQAGGQGGGAPSNQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
287_21 50 KEDAPQAGGQGGGAPSNQGGQDMAAVSEENTGNGGAVTADNPKNEDEVAQNDMPQNAAGT
z2491 50 KEDAPQAGGQGGGAPSNQGGQDMAAVSEENTGNGGAVTADNPKNEDEVAQNDMPQNAAGT
287_9 61 VSGAPQADT...QDATAGGQDMAAVSAENTGNGGAATDNPKNDEGFQNDMPQNAADT
fa1090 61 AGGAPQADT...QDATAGGQDMAAVSAENTGNGGAATDNPKNDEGAQNDMPQNAADT

287_14 110 DSLTPNHTPASNMPAGNMCNOAPDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
287_2 110 DSLTPNHTPASNMPAGNMCNOAPDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
287_21 110 DSSTPNHTPDNMLAGNMCNOATDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
z2491 110 DSSTPNHTPDNMLAGNMCNOATDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
287_9 119 DSSTPNHTPDNMPTRDMCNOAPDAGESEQPANQPDMAANTADGMOGDDPSAGGENAGNTA
fa1090 117 .....

287_14 170 AQSTNOALNNQTAGSQNPASSTNPSTNSGGDEGRITNTNSV...IDGPSQNTLTHCKGDS
287_2 170 AQSTNOALNNQTAGSQNPASSTNPSTNSGGDEGRITNTNSV...IDGPSQNTLTHCKGDS
287_21 170 AQSTNOALNNQTAGSQNPASSTNPSTNSGGDEGRITNTNSV...IDGPSQNTLTHCKGDS
z2491 170 AQSTNOALNNQTAGSQNPASSTNPSTNSGGDEGRITNTNSV...IDGPSQNTLTHCKGDS
287_9 178 DQSTNOALNNQTAGSQNPASSTNPSTNSGGDEGRITNTNSV...IDGPSQNTLTHCKGDS
fa1090 117 .ESANQTCNNOPAGSSDSAPASNPAPANGGSDGGRITNTNSV...IDGPSQNTLTHCKGDS

287_14 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKKDGKNDGKNTK...FVGLVADS...VOMKGINOYII
287_2 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKKDGKNDGKNTK...FVGLVADS...VOMKGINOYII
287_21 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKK...DGKNTK...FVGLVADS...VOMKGINOYII
z2491 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKK...DGKNTK...FVGLVADS...VOMKGINOYII
287_9 238 CDRD...FLDEEAPPKSEFEKLSDAKISNYKK...DGKNTK...FVGLVADS...VOMKGINOYII
fa1090 176 CNGDNLDEEAPPKSEFEKLSDAKISNYKK...DGKNTK...FVGLVADS...VOMKGINOYII

287_14 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_2 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_21 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
z2491 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_9 293 IYKDKSAS...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
fa1090 232 FYTDKPT...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPS...PGRFAA
287_2 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPS...PGRFAA
287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPS...PGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPS...PGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPS...PGRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPS...PGRFAA

287_14 408 KVDFGSKSVDCIIDSGLHMGTKQFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
287_2 408 KVDFGSKSVDCIIDSGLHMGTKQFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
287_21 404 KVDFGSKSVDCIIDSGLHMGTKQFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
z2491 404 KVDFGSKSVDCIIDSGLHMGTKQFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
287_9 413 KVDFGSKSVDCIIDSGLHMGTKQFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
fa1090 345 KVDFGSKSVDCIIDSGLHMGTKQFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA

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FIG. 21A

287_14	468	GKYSYRPTDAEKGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGFGVFAGKKEQD*

FIG. 21B


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z2491_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR

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z2491_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
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zv21_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

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z2491_519 301 ISAGMKIIDSSKTA*
zv26_519 301 ISAGMKIIDSSKTA*
zv22_519ass 301 ISAGMKIIDSSKTA*
fa1090_519 301 ISAGMKIIDSSKTA*
zv32_519 301 ISAGMKIIDSSKTA*
zv11_519 301 ISAGMKIIDSSKTA*
zv28_519 301 ISAGMKIIDSSKTA*
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zv21_519ass 301 ISAGMKIIDSSKTA*
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zv20_519ass 301 ISAGMKIIDSSKTA*
zv06_519ass 301 ISAGMKIIDSSKTA*
zv29_519ass 301 ISAGMKIIDSSKTA*

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Fig. 22B

Fig. 23A

Fig. 23B

Fig. 23C

fa1090	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc	361	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMKPEYRP
zm33asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm32asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm23asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm27bc	421	QKTTGYVWQLLPNGMKPEYRP
zm09	421	QKTTGYVWQLLPNGMKPEYRP
zm10	421	QKTTGYVWQLLPNGMKPEYRP
zm24	421	QKTTGYVWQLLPNGMKPEYRP
zm25	421	QKTTGYVWQLLPNGMKPEYRP
zm14	421	QKTTGYVWQLLPNGMKPEYRP
zm04	421	QKTTGYVWQLLPNGMKPEYRP
zm11asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm08n	421	QKTTGYVWQLLPNGMKPEYRP
zm96	421	QKTTGYVWQLLPNGMKPEYRP
zm01	421	QKTTGYVWQLLPNGMKPEYRP
zm02	421	QKTTGYVWQLLPNGMKPEYRP
zm03	421	QKTTGYVWQLLPNGMKPEYRP
zm07	421	QKTTGYVWQLLPNGMKPEYRP
zm12	421	QKTTGYVWQLLPNGMKPEYRP
zm18	421	QKTTGYVWQLLPNGMKPEYRP
zm19	421	QKTTGYVWQLLPNGMKPEYRP
zm20	421	QKTTGYVWQLLPNGMKPEYRP
zm21	421	QKTTGYVWQLLPNGMKPEYRP
zm06	421	QKTTGYVWQLLPNGMKPEYRP
zm17	421	QKTTGYVWQLLPNGMKPEYRP
zm13	421	QKTTGYVWQLLPNGMKPEYRP
zm05	421	QKTTGYVWQLLPNGMKPEYRP
z2491	421	QKTTGYVWQLLPNGMKPEYRP
zm22	421	QKTTGYVWQLLPNGMKPEYRP
zm26	421	QKTTGYVWQLLPNGMKPEYRP
zm28	421	QKTTGYVWQLLPNGMKPEYRP
zm29asbc	421	QKTTGYVWQLLPNGMKPEYRP
zm16	421	QKTTGYVWQLLPNGMKPEYRP
zm15	421	QKTTGYVWQLLPNGMKPEYRP
zm31asbc	421	QKTTGYVWQLLPNGMKPEYRP

Fig. 23D